


```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: 50C
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGEM-11 library of L. Poncerrada
; CLONE: 50C(b)
; US-08-315-468-4

Query Match          20.4%; Score 745; DB 1; Length 1169;
Best Local Similarity 29.4%; Pred. No. 1.1e-56;
Matches 217; Conservative 142; Mismatches 274; Indels 104; Gaps 31;

Qy  4 MSPYQNKNEYEILBS--SSNNTNTPNRYPPAN--NRDMSTSMWDCQGIS-----W 50
    |||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  1 MSP-NNQNEYEIIDATPSTSVSDNSRYPPANEPTNALQNMWDYKYLKMSAGNVSYPEGS 59

Qy  51 DETWESVETITSGINLIEPVIE---PSLGGINTILS-IIGKLIPNRTQVTSALSTCDL 105
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  60 PEVFLSQDQAVKAAIDVGLKLTGLGVFPFIVSLYQTLFDILWPQSKQSQWEIFMEQV 119

Qy  106 LSIIRKEVADSVLSDAIDFQGLKNTREYVLSYLGAWLKD---GKPLQKTNSNDIGOLV 162
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  120 EELNQKIAEVARNKALSEGLEGNYY-QLYLTALEEMKENPNSGRALRDVNR----- 172

Qy  163 YPKLSERDPNEILGGSLSRNNQVLLPPTAQANVOLLLLRDAVOYKQAWFPFLSAEN 222
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  173 --FEILDSLFQYV-PSFRVTNPEVPFLTVYTWAANLHLLLRDASIFGEEW--GLSTST 227

Qy  223 VRSELISPNSGCDFTGDIYERLCKTAEYTNLYQVGLNQIKQGTGADTWSKENKF 282
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  228 I-----NNYNRQMKLTAEYSDHCVKVETGLAKLK--GSSAKQWIDNQF 271

Qy  283 RREWTLAVLDIIAIFPYDFPEKYPPLTHVELTREIYTDVAGYSS--GTYGWLNRWNPFTN 340
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  272 RREMTLTVDLWALFNSYDTRTYPLATTATQLTREVTYDPLGAVDVPNIGSWYDKAP-SFS 330

Qy  341 GLEANGTRGGLVTWLSKIGIYNEYVS---RYPAGWVGRTHVEDYTKGNCIFORMSGTT 396
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  331 EIEKAALRPPHVPFDITGLTVYTKGRFTSDRYWYAGHQISYKHIGTSTFTQMTGTN 390

Qy  397 SN--DLRNIQDNADVYKITS--LAIMNLVGETTARPEYRVSKADFRVG-----GPDLN 447
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  391 QNLQSTSNFDFTNYDIYKTLNSGAVLLDVIYVPGYTYTFPGPETEFEPWVQLNTRKTLT 450

Qy  448 YDAGNNGLSRMTIESTPVLVHSG---VRGSPHRLSNAACVVYGNR---VNVYGHWTHT 501
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  451 YKPASKDIIDRTDSELELPETSPGQNPYSYSHRLGHIT-FIYSSSTSTVVPVFSWTHR 509

Qy  502 SLKRENIIEANQITQIPAVKSYVLQNYLANAYTVIKGT-HTGGDLRRLFLT--KSRYNA 558
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  510 SADLTNTVKSGETIQIPGKKSITI-----GRNTYIIKRGVYTGCDIVALTDIGSCCFQM 564

Qy  559 VYAGCGIRLIINNKTAGQSTRIPRYAADKAAFPFVLYPGCGNSRNFVLEKSYSG-NY 617
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  565 IF-----PESQREPRIRIYASNETSYISLY---GLNQSGTLKFNQOTYSKNKE 608

Qy  618 DDLKYSDFKFAEIIITPPLSPSNIQMDVEMOANGFQSDVNV-VLDKIBFLPSNTTLLRYEG 676
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db  609 NDLTYNDFKIEV--PRVISVNASNNIQRISIGIQTNLTNFIILDRIEFIPVDET---YEA 663

Qy  677 ERDELEKTNKAVNDLFTN 693
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Db  664 ETDLEAKKAVNALFTN 680
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```

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; Patent No. 5359048
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwabana, Hidenori
; APPLICANT: Sato, Reiichi
; APPLICANT: Suzuki, NO. 5359048ukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasaki, Tadaaki
; TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,203
; FILING DATE: 19920723
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-915-203-2

Query Match          19.9%; Score 728.5; DB 1; Length 1149;
Best Local Similarity 29.9%; Pred. No. 3.2e-55;
Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34

Qy      4 MSPYQNKEYEILBSSNNNTWPN--RYPFANRDMSTMWNDCOGISWDE----- 52
Db      1 MSP-NNQYEIIDLSPTSVSDNSIRYPLANDQTNLQNMNYKDYLKWTESTNAELSRN 59
Qy     53 --TWESVETTSIGINIEFVIE----PSLGINTLL-SITGKLPTNRQTVSALSIDCL 105
Db      60 PGTFSIAQDAVGTDIVSTIIISGLGIPVLGEVFSILGSLIGLLWPSPNNENVMQIFMNRV 119
Qy    106 LSIIRKEVADSVLSDAADPGKLKNYR---EYLYSLYGAWLKCKGPKLQKTNNSDIGQLV 162
Db    120 BELDQKILDSVRSAIAD----LANSRIAVEYYQNALEDWRKNP---HSTRSAAU----- 168
Qy    163 YYPFKLSERDFN--EILG---GSLSRNNAQVLLLPFFAQAANVQLLLRLLDVAVQYKAQWFPF 217
Db    169 ----VKERFGNAEAILATNMGPSQTNVETPLLPYQAASLHLVLMRDVQIYKEWG-- 222
Qy    218 LSAENVRSSELSPNSGCDFGTGDYVERLUKCKTAETYNYCLYWVQVGLNQIKCGGTGADTWS 277
Db    223 -----YPQNDIDL---FYKEQVSYTYARYSDHCVCQWYNAGINKLR--GTGAQKWV 266
Qy    278 KENKREMTLAVLDIITAIPPYDPKYPLPTHVELTREIYTDVAG-YSSGYTYSMLRNWP 336
Db    267 DYNRFRMMVMVDLVALLFPNYDARIYPLSTNAELTREIFDDPVGSYVTGQSSTLISWY 326
Qy    337 N-----TFNGLEANGTRGFGLVTWLISKGIYNEY-----VSRYFAGWGTGRHYEDYTKG 385

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```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1156 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-002-285-70

Query Match          20.4%; Score 747; DB 2; Length 1156;
Best Local Similarity 30.6%; Pred No. 7,3e-57;
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

QY 9 NKNYEILESSNNTNTPN--RYPPANNRDMSTMWNCQCG---ISW-DEIWESVETITTS 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 NONKHGIIGASCGCASDDVAKYPLANNPYSSALNLSQNSILLNWINIIGDAAKEAVS 61

QY 63 IGINLIEFVIPSICG-INTLLSIIGKLI-PTNQTVSALSICDLSIIRKEVADSVLSD 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 IGTITVSLITAPSLTGLISIVYDLIGKVGSSGQSISDLSICDLSIIDLRVSQSVLND 121

QY 121 ATADFDGKLNKRYEYLSVLGAWLKDGKPLQKTNNSDIGLVYVFKLSERDFNEIL---- 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 GIADFNQSVLLYRN-YLEALDSWNKN-----PNSASAEELRTPRIADSEFDRLITRGS 174

QY 177 ---GGSLSRNNAQVLLPTFAQANVQLLLLRDAVQYKAQW-----FPFLSAENVRSBLI 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
175 LTNGGSLARQNAQIILLPSFASAAFFHLLLRDATRYGTNNGLYNATPFINYQSKLVELI 234

QY 229 SPNSGCDFTGDIYERLCKTAEYTNCLYWTQVGLNQIKOGGTGADTWSKKNKPREMTL 288
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 E-----LYTDCVHWYNRGNFELRQRTSATAWLEFHRYRREMTL 274

QY 289 AVLDDIIAIFTPTDFEYKYPVLPHTHVELTREIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342

; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1156 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-589-477-70

Query Match          20.4%; Score 747; DB 2; Length 1156;
Best Local Similarity 30.6%; Pred No. 7,3e-57;
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

QY 9 NKNYEILESSNNTNTPN--RYPPANNRDMSTMWNCQCG---ISW-DEIWESVETITTS 62
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 NONKHGIIGASCGCASDDVAKYPLANNPYSSALNLSQNSILLNWINIIGDAAKEAVS 61

QY 63 IGINLIEFVIPSICG-INTLLSIIGKLI-PTNQTVSALSICDLSIIRKEVADSVLSD 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 IGTITVSLITAPSLTGLISIVYDLIGKVGSSGQSISDLSICDLSIIDLRVSQSVLND 121

QY 121 ATADFDGKLNKRYEYLSVLGAWLKDGKPLQKTNNSDIGLVYVFKLSERDFNEIL---- 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 GIADFNQSVLLYRN-YLEALDSWNKN-----PNSASAEELRTPRIADSEFDRLITRGS 174

QY 177 ---GGSLSRNNAQVLLPTFAQANVQLLLLRDAVQYKAQW-----FPFLSAENVRSBLI 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
175 LTNGGSLARQNAQIILLPSFASAAFFHLLLRDATRYGTNNGLYNATPFINYQSKLVELI 234

QY 229 SPNSGCDFTGDIYERLCKTAEYTNCLYWTQVGLNQIKOGGTGADTWSKKNKPREMTL 288
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 E-----LYTDCVHWYNRGNFELRQRTSATAWLEFHRYRREMTL 274

QY 289 AVLDDIIAIFTPTDFEYKYPVLPHTHVELTREIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
275 MVLDIVASFSSLDITNYFIETDFQLSRVIYTDPIGFVRSSLRGSWFSFVNRA--FSDL 333

QY 343 EANGTRGPGVLTWLSKIGIYNEVYSRYFAG-----WVGTTRYEDYTKGNGIFORMSGT 395
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
334 E-NAIPNPRPSWFLNMIISTGSLTLPVSPSTRARVMYGSRRDRISPANSQFTELISGQ 392

QY 396 TSNDLNRNIDFQNAVYKITSALMILVGETTARPYRSKADPRVGGPDNLNAGNGL 455
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
393 HTTATQTILGRN--IFRVDQA--CNL-NDTT----YGVNRAVF-----YHDASEGS 435

QY 456 SMTIESTFPPLVHSGNVRGP-----SHRLSNAACVVYV----- 489
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
436 QRSVVEG-----YIRTGIDNPRVQNTIYLPQNSDIPEDYTHILSTINTLGTGLRQV 491

QY 490 ---NSRVNVYGWTHSLKRENIIEANOITQIPAVKSYLQNLANAYTVYIKGTHTCGD 545
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
492 ASNRSSSLVMYGWTHSKLARNTNTPDRITQIPLTK----VDTRGTGVSYVNDPGFIGA 547

QY 546 LIRFLRTKSEYNAVAGGIRLIIINNKTAGQSYRIRFRYAADKAFFSVLYPGWGNR 605
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
548 LLQ-----KTDHGS-----GVLRVQFPLHLRQOQYRIRVYASTNIRLSV-----NGS 591

QY 606 FVSLSKSYSGNY---DDLKYSDFKAEIITPPLP--SSNIQMDEVMOANSFQSDVNVVLDK 661
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
592 FGTISQNLPSWRLGEDLYGSFAIREFNSTIRPTASPDQIRLTETPFIQREVYV--DR 649

QY 662 IEFLPSNTTTLLEYGERDLKTKNAVNDLFT 692
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 IEFIPVNPTR---EAKEDLEAAKAVASLFT 677

RESULT 5
US-09-589-477-70
; Sequence 70, Application US/09589477
; Patent No. 6570005
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Db 598 GGQSVNMPLQKMEIGENLTSTRFYTFDSNPFSPRANPDI--IGISEQPLFGAGSISS 655
Qy 654 DVNVVLDDKIEFLSNNTTILEYGEERDLKTKNAVNDLFTN 693
Db 656 G-BLYIDKIEIILADAT---FEAESDLERAQKAVNALFTS 691

RESULT 3

US-09-001-982-10
; Sequence 10, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-001-982-10

Query Match 20.4%; Score 747; DB 2; Length 1156;
Best Local Similarity 30.8%; Pred. No. 7.3e-57;
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

Qy 9 NKNEYEILSSNNNTNPN--RYPFANNRDMSTMWDCQG---ISW-DEIVESVETITS 62
Db 2 NQNKHGIIGASNGCGASDDVAKPLANNPYSSALNLSNCSILNWINIIGDAKAEVS 61
Qy 63 IGINLIEFVIERSLGG-INTLISIIIGKLI-PTNRQTVSALSICDLISIRKEVADSVLSD 120
Db 62 IGTIVSLTAPSLTGLSIVVDLICKVLGGSGQISDLSICDLLSIIDLVSQSVLND 121
Qy 121 ATADPGKLNTRYLYSLVIGLAWLKDGKPLQKTNNSDQGLVYVFKLSERDFNEIL---- 176
Db 122 GIADFNGSVLLYRN-YLEALDSWNKN-----PNSASAEELRTRFRIADSEFDRILTRGS 174
Qy 177 ---GGSLRNNAQVLLPTFAOAAVQLLLRLDAVOYKAQW-----FPLSAENVRSLEI 228
Db 175 LTNQGLSLAQNAQIILLPSFASAFPHLULLLRLDARTYGNWGLYNATPINTQSKLVELI 234
Qy 229 SPNSGCDFTGDYERLCKTAEYTNVCLYQVQVLNQIKQGGTGADTWSKFNKFRREMTL 288
Db 235 E-----LYTDYCVHWYNRGNFELRQRTGSATAWLEFHYRREMTL 274

Qy 289 AVLDDIATPTDYFEKYPLEPHVELTREIYTDVGY-----SSGTYSWHLR--NHPNTNGL 342
Db 275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNRA--FSDL 333
Qy 343 EANGTRGPGLVTLWSKIGIYNEVSVRFAG-----WVCTRHYEDYTKNGIFORMSGT 395
Db 334 E-NAIENPRPSWFLNNMIISTGSLTLPVSPSTDRARVWYGSRRDIRSPANSQFTTELISGQ 392
Qy 396 TSNLRLNIDFQNAVYKITS LAIMNLVGETTARPEYRVSKADFRVVGPDNLNDAGNGL 455
Db 393 HTTATQTILGRN--IFRVDQA-CNL-NDTT-----YGVNRAVF-----YHDASEGS 435
Qy 456 SRMTIESTPFLVLHNSGVGRP-----SHRLSNAACVVYVY-----489
Db 436 QRSVYEG---YIRTTGIDNPRVQNTYLPGENSDIPTEDYTHILSTTINLTGSLRQV 491
Qy 490 ---NSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYVLYQLNLANAYTVIKGTHGGD 545
Db 492 ASNRSSLLVMYQWTHKSLARNNTINPRITQIPLTK-----VDRGTGVSIVNDPFGFIGGA 547
Qy 546 LIRFLRTKSEYNAVYAGGIRLIINNKTAGQSYRIRFYAADKAAFFSVLYLPGMGSNR 605
Db 548 LLQ-----RTDHGSL---GVLRVQPLHLRQQYRIRVRVASTTNRILSV-----NGS 591
Qy 606 FVSLEKSYSGNY---DDLKYDFKFAEIIITPPLP-SSNIQMDVEMQANSFQSDVNVVLDK 661
Db 592 FGTISQNLFPSTWRLGEDLYGSAIFRENTSIRPTASPDQIRLTIRPFIQEVYV--DR 649
Qy 662 IEFPLSNTTILEVEGERDLEKTKNAVNDLFT 692
Db 650 IEFIPVNPTR---EAKEDLEAAKAVASLFT 677

RESULT 4

US-09-002-285-70
; Sequence 70, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2

63 IGINLIEFVIEPSLGG-INTLLSIIIGKLI-PTNRQTVSALSICDLSIIIRKEVADSVLSD 120
62 IGTIVSLIAPSLTGLSIVYDLIGKVLGGSSQSIDLSICDLSIIDURVQSGLND 121
121 AIADFDGKLNRYEYLSYLGAWLKGDPLOKTNNSDIGQLVYVYFKLSERDFNEIL- 176
122 GIADFNGLVLYRN-VLEALDSWKN-PSASAEELRTRFRIADSEFDRLTRGS 174
177 ---GGSLSRNAQVLLPTFAQANVQLLLRDADVOYKAQW-----PFLSAENVRSLEI 228
175 LTNGGSLARQNAQIILLPSFASAFHLLLRDADRYGTNMGLYNATPFINYQSKLVELI 234
229 SPNSGCDFTGDYERLCKTAEYNYCLYVQVGLNOIKQGTGADTWSKKNKPRREMTL 288
235 E-----LYTDYCVHWYNRGNELRQRTSATWLEFHYRREMTL 274
289 AVLDIILAIPTDYFPEKYPPLTHVELTRIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342
275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGVHRSRLRGESWFSFVNRRAN-FSDL 333
343 BANGTRGGLVTLWSKIGIYNEYSRYFAG-----WVGTRHYEDYTKNGIFORMSGT 395
334 E-NAIPNRPSPFLNNMIISTGSLTPVSPSTDRARVWYGSRRDRISPANSQFITEISGQ 392
396 TSNDLRNIDFONADVYKITSIAIMNLVGETTARPEYRVSKADFRVRGPDLYDAGNGL 455
393 HTTATQITLGRN--IFRVDQA-CNL-NDTT-----YGVNRAVF-----YHDASGGS 435
456 SRMTIESTFPLVHLSNGVRGP-----SHRLSNAACVVYV----- 489
436 QRSVVEG---YIRTTGIDNPRVQNTYLPGENSDIPTPEDYTHILSTINTLTGLRQV 491
490 ---NSRVNVYGTWHTSLKRENIIEANQITQIPAKSYLYQLYLANATYVIKGT-HTGG 544
492 ASNRSSSLVMYGTWHTSLKRENIIEANQITQIPAKSYLYQLYLANATYVIKGT-HTGG 546
545 DLIRFLRTKSEYNAVYAGGIRLIIN-NKTAGQSVRIIRFVAAADKAFFSVLYPGGWS 603
547 DILR-----RNTF-----GDFVSLQVNIINSPTQIRLFRFVASSRDARVILVTGAASGV 597
604 NRVFSLEKSYSGNYD-----DLKYSDFK--FAEITPPLPSSNIQMDVEMQANSFQS 653
598 GQGVSNVPLQKTMIEGENTLSRTFRYTDPSNPFSPFRANPDI--IGISEQPLFGAGSISS 655
654 DVNVVLDKIEPLSPNTTILEYEGERDLEKTKNAVNDLFTN 693
656 G-ELYDKIEITLADAT---FEASDLERAQKAVNALETS 691

RESULT 2

US-09-668-650-12

Sequence 12, Application US/09668650

Patent No. 6780408

GENERAL INFORMATION:

APPLICANT: Boesch, Hendrick J.

TITLE OF INVENTION: Hybrid toxin

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSER: No. 6780408artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/668,650

FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-668-650-12

Query Match 20.9%; Score 762.5; DB 2; Length 1242;
Best Local Similarity 31.2%; Pred. No. 3.4e-58;
Matches 237; Conservative 126; Mismatches 252; Indels 145; Gaps 33;
QY 9 NKNYEILESSNNNTNPN--RYPPANNRDMSTWSDCCQ---ISW-DETWESVETITS 62
DB 2 NQNHGIIAGSCGASDDVAKYPLANNPYSSALNLSQNSSSILNWINIIGDAAKEAVS 61
QY 63 IGINLIEFVIEPSLGG-INTLLSIIIGKLI-PTNRQTVSALSICDLSIIIRKEVADSVLSD 120
DB 62 IGTIVSLIAPSLTGLSIVYDLIGKVLGGSSQSIDLSICDLSIIDURVQSGLND 121
QY 121 AIADFDGKLNRYEYLSYLGAWLKGDPLOKTNNSDIGQLVYVYFKLSERDFNEIL- 176
DB 122 GIADFNGLVLYRN-VLEALDSWKN-PSASAEELRTRFRIADSEFDRLTRGS 174
QY 177 ---GGSLSRNAQVLLPTFAQANVQLLLRDADVOYKAQW-----PFLSAENVRSLEI 228
DB 175 LTNGGSLARQNAQIILLPSFASAFHLLLRDADRYGTNMGLYNATPFINYQSKLVELI 234
QY 229 SPNSGCDFTGDYERLCKTAEYNYCLYVQVGLNOIKQGTGADTWSKKNKPRREMTL 288
DB 235 E-----LYTDYCVHWYNRGNELRQRTSATWLEFHYRREMTL 274
QY 289 AVLDIILAIPTDYFPEKYPPLTHVELTRIYTDVAGY-----SSGTYSWLR--NWPNTFNGL 342
DB 275 MVLDIVASFSSLDITNYPIETDFQLSRVIYTDPIGVHRSRLRGESWFSFVNRRAN-FSDL 333
QY 343 BANGTRGGLVTLWSKIGIYNEYSRYFAG-----WVGTRHYEDYTKNGIFORMSGT 395
DB 334 E-NAIPNRPSPFLNNMIISTGSLTPVSPSTDRARVWYGSRRDRISPANSQFITEISGQ 392
QY 396 TSNDLRNIDFONADVYKITSIAIMNLVGETTARPEYRVSKADFRVRGPDLYDAGNGL 455
DB 393 HTTATQITLGRN--IFRVDQA-CNL-NDTT-----YGVNRAVF-----YHDASGGS 435
QY 456 SRMTIESTFPLVHLSNGVRGP-----SHRLSNAACVVYV----- 489
DB 436 QRSVVEG---YIRTTGIDNPRVQNTYLPGENSDIPTPEDYTHILSTINTLTGLRQV 491
QY 490 ---NSRVNVYGTWHTSLKRENIIEANQITQIPAKSYLYQLYLANATYVIKGT-HTGG 544
DB 492 ASNRSSSLVMYGTWHTSLKRENIIEANQITQIPAKSYLYQLYLANATYVIKGT-HTGG 546
QY 545 DLIRFLRTKSEYNAVYAGGIRLIIN-NKTAGQSVRIIRFVAAADKAFFSVLYPGGWS 603
DB 547 DILR-----RNTF-----GDFVSLQVNIINSPTQIRLFRFVASSRDARVILVTGAASGV 597
QY 604 NRVFSLEKSYSGNYD-----DLKYSDFK--FAEITPPLPSSNIQMDVEMQANSFQS 653
DB 598 GQGVSNVPLQKTMIEGENTLSRTFRYTDPSNPFSPFRANPDI--IGISEQPLFGAGSISS 655


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QY 106 LSIIRKEVADSVLSDAIADFDGKLNRYEYLSYLGAWLKD-----GKPLQKTN 155
Db 120 EELINQKIAEYARNKALSEGLGNNY-QLYLTALBEEENPFRSRGPRSRGALRDVRN 178
QY 156 SDIGOLVYVFKLSERDFNEILGGLSLSRNNAAVLLPTFAQANVOLLRLDVAQVKAQWF 215
Db 179 R-----FEILDSLFTQYM-PSFRVTNFEVFPFLTVYMAAANLHLLKDAIFGEBW- 228
QY 216 PFLSAENVRSSELISPNSCDFT--GDYERLCKTAETNYCLYQVGLNQIKOGGTGA 273
Db 229 -----GWSTTTNNYDQMKLTAEYSDHCVKWEYETGLAKLK--GTSA 269
QY 274 DTWSKFNKFRREMTLAVLDIIAIPFYDEKYPPLTHVELTREIYTDVAG--YSGGTYSW 331
Db 270 KQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSW 329
QY 332 LRNPNTFNGLEANGTRGPGLVTLWLSKIGIYNEYS---RYFAGWVQTR-HYEDYTKGN 386
Db 330 YDKAP-SFGVIESSVIRPPHVPDYITGLTVYTSQRSISSARYIRHWAGHOISYHRVSRGS 388
QY 387 GIFORMSGTTSN--DLRNIQFONADVYKITS--LAIMNLVGETTARPEYRVSKADPRVVG 442
Db 389 NL-QQMYGTGNLHSTSTFDFTNYDIYKTLSDAVLLDIV-----YPGY-----TYIFPG 437
QY 443 GPDLYNDAGN-----NGLSRMTIESTF-----PLVLHNSGVRGSPSHLSNAA 484
Db 438 MPEVEFFWVNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQPNYESYSHRLCHIT 497
QY 485 CV-VYGNR--VNVYGTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVYIKGT- 540
Db 498 SIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKWCW--DNL---PPVPVVKGP 552
QY 541 HTGGDLIRFLRTKSEYNAYV-AGGGIRLIINNKTAGQSYRIRFRYAADKAAPFSVLYPG 599
Db 553 HTGGDLQYNRSTGSGVTLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV----- 602
QY 600 GWSNRFRVLSLEKSYSGNYDDLKYSDFKFAEIIITPPLPSSN-----IQMDVEMQANSFQSDV 655
Db 603 ---NDAQIQMPKTMNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHNVGDPNSTLSGI 658
QY 656 NVVLDKIEFLPSNTTLEYEGE 677
Db 659 -VYVDRIEFIPVDET---YEAE 676

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RESULT 15

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US-11-108-389-40
; Sequence 40, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 40

```

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; LENGTH: 676
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-40

Query Match
Best Local Similarity 29.1%; Pred. No. 4.2e-45; Length 676;
Matches 216; Conservative 138; Mismatches 254; Indels 134; Gaps 37;

QY 4 MSPYONKNEYEILS--SSNNTNTPNRYPPAN--NRDMSTWMDCCOIS-----W 50
Db 1 MSP--NNQNEYEIIIDATPSTSVSNDNSRYPFANEPTNALQNMNDYKDYLKMSAGNASEYPGS 59
QY 51 DEIWESVETITISGINLIEFVIE---PSLGGINTLLS-IIGKLIPTRQTVSALSICDL 105
Db 60 PEVLVSQDAAKAADIVGKLSGLGVFPVGPVLSVLTQLDILWPSEKESQWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIADFDGKLNRYEYLSYLGAWLKD-----GKPLQKTN 155
Db 120 EELINQKIAEYARNKALSEGLGNNY-QLYLTALBEEENPFRSRGPRSRGALRDVRN 178
QY 156 SDIGOLVYVFKLSERDFNEILGGLSLSRNNAAVLLPTFAQANVOLLRLDVAQVKAQWF 215
Db 179 R-----FEILDSLFTQYM-PSFRVTNFEVFPFLTVYMAAANLHLLKDAIFGEBW- 228
QY 216 PFLSAENVRSSELISPNSCDFT--GDYERLCKTAETNYCLYQVGLNQIKOGGTGA 273
Db 229 -----GWSTTTNNYDQMKLTAEYSDHCVKWEYETGLAKLK--GTSA 269
QY 274 DTWSKFNKFRREMTLAVLDIIAIPFYDEKYPPLTHVELTREIYTDVAG--YSGGTYSW 331
Db 270 KQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSW 329
QY 332 LRNPNTFNGLEANGTRGPGLVTLWLSKIGIYNEYS---RYFAGWVQTR-HYEDYTKGN 386
Db 330 YDKAP-SFGVIESSVIRPPHVPDYITGLTVYTSQRSISSARYIRHWAGHOISYHRVSRGS 388
QY 387 GIFORMSGTTSN--DLRNIQFONADVYKITS--LAIMNLVGETTARPEYRVSKADPRVVG 442
Db 389 NL-QQMYGTGNLHSTSTFDFTNYDIYKTLSDAVLLDIV-----YPGY-----TYIFPG 437
QY 443 GPDLYNDAGN-----NGLSRMTIESTF-----PLVLHNSGVRGSPSHLSNAA 484
Db 438 MPEVEFFWVNLNTRKTLKYNPVSKDIIASTRDSLELPPETSQPNYESYSHRLCHIT 497
QY 485 CV-VYGNR--VNVYGTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVYIKGT- 540
Db 498 SIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKWCW--DNL---PPVPVVKGP 552
QY 541 HTGGDLIRFLRTKSEYNAYV-AGGGIRLIINNKTAGQSYRIRFRYAADKAAPFSVLYPG 599
Db 553 HTGGDLQYNRSTGSGVTLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV----- 602
QY 600 GWSNRFRVLSLEKSYSGNYDDLKYSDFKFAEIIITPPLPSSN-----IQMDVEMQANSFQSDV 655
Db 603 ---NDAQIQMPKTMNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHNVGDPNSTLSGI 658
QY 656 NVVLDKIEFLPSNTTLEYEGE 677
Db 659 -VYVDRIEFIPVDET---YEAE 676

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Search completed: December 15, 2005, 11:21:11

Job time : 14 secs

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Db 561 RSTGSGVTGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQIOM 607
QY 610 EKSYSGNYDLKYSDPKFABIITPPLPSN-----IQMDVEMQANSFQSDVNVVLDKIEFL 665
Db 608 PKTMNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHVNGEDPNSTLSGI-VYVDRIEFI 665
QY 666 PSNTTTLLEYEGE 677
Db 666 PVDET---YEAE 674

RESULT 13
US-11-108-389-50
; Sequence 50, Application US/111108389
; Publication NO. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-50

Query Match 18.1%; Score 660; DB 7; Length 674;
Best Local Similarity 29.1%; Pred. No. 4.2e-45;
Matches 213; Conservative 141; Mismatches 262; Indels 116; Gaps 35;

QY 4 MSPYONKNEVEILES--SSNNTNTPNRYFPAN--NRDMSTMSWNCQGIS-----W 50
Db 1 MSP-NNQNEYIIDAFTSTSVNSDNRYPFANEPTNALQNMDYKYLKMSAGNASSEYPS 59
QY 51 DEIWESVETITSGINLIEFVIE---PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLVFPVGPVIVSLYTLQILILWPSGKESQWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIADPDGKLKNRYEYISYLGAWLKDGKPLQKTNNSDIGQLVYVF 165
Db 120 EELINQKIAEYARNKALSLEGLGNNY-QLYLTALREWEENPNFSRFRQALRDVRNRF 178
QY 166 KLSRDFNEILGSLSRNNAQVLLPTFAQANVOLLILRDADAVQYKAQWFPFLSAENVRS 225
Db 179 EILDSUFTQYM-PSFRVTFVFPFLTVYAMAANLHLLLKDASIFGEW----- 226
QY 226 ELISPNSGCDFT--GDYERLACKTAETNYCLYWYQVGLNQIKOGGTGADTWKSNFKPR 283
Db 227 -----GWSTTINNYDROMKLTAEYSDHCVKWVETGLAKL--GTSAKQWVDYNQPR 277
QY 284 REMTLAVLDIIAIFPYDEKYPPLPHVELTREIYTDVAG--YSGGTYSWLNRWPNFTNG 341
Db 278 REMTLAVLDVAVLFPNYDTRTPMETKAQLTREYTDPLGAVNVNVSIGSWYDKAP-SFGV 336
QY 342 LEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVGTR-HYEDYTKNGIFQRMSTGT 396

```

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Db 337 ISSVIRPPHVDYITGLTVYITQSRSSISSARYIRHWAGHOISYHRVSRGSNL-QQMYGTN 395
QY 397 SN--DLRNIDFQADVYKITS--LAIMNLVGETTARPEYRVSKADPRRVGGPDPLANTDAGN 452
Db 396 QNLHSTSTDFNTYDIYKTLSDKDAVLDDIV-----YPGY-----TVIFFGMEVEFPMVN 445
QY 453 -----NGLSRMTIESTP-----PLVLHNSGVGRGSHRSLUSNAACV-VYQNSR- 492
Db 446 QLNNTKRLKYNPVSXKDIIASTRDSLELPPESTDQPNYESYSHRLCHITSIPATGNTTG 505
QY 493 -VNVYGWHTSLKRENIIEANOITQIPAVKSYVLQNYLANAYTYVIKGT-HTCGDILIFL 550
Db 506 LVPFVSWTHRSADLNNITYSDKITQIPAVKCM--DNL-----PFPVVVKGPGHTGGDLLQVN 560
QY 551 RTKSEYNNAVY-AGGGIRLIINNKTAGQSRYIRFRVAADKAAFFSVVLYPGMGSGNRFVSL 609
Db 561 RSTGSGVTGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQIOM 607
QY 610 EKSYSGNVDDLYKSDPKFABIITPPLPSN-----IQMDVEMQANSFQSDVNVVLDKIEFL 665
Db 608 PKTMNPG-EDLTSKTFKVADAITTVNLATDSSVAVKHVNGEDPNSTLSGI-VYVDRIEFI 665
QY 666 PSNTTTLLEYEGE 677
Db 666 PVDET---YEAE 674

RESULT 14
US-11-058-727-40
; Sequence 40, Application US/11058727
; Publication NO. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-40

Query Match 18.1%; Score 660; DB 7; Length 676;
Best Local Similarity 29.1%; Pred. No. 4.2e-45;
Matches 216; Conservative 138; Mismatches 254; Indels 134; Gaps 37;

QY 4 MSPYONKNEVEILES--SSNNTNTPNRYFPAN--NRDMSTMSWNCQGIS-----W 50
Db 1 MSP-NNQNEYIIDAFTSTSVNSDNRYPFANEPTNALQNMDYKYLKMSAGNASSEYPS 59
QY 51 DEIWESVETITSGINLIEFVIE---PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAAKAADIIVGKLLSGLVFPVGPVIVSLYTLQILILWPSGKESQWEIFMEQV 119

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; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-50

Query Match 18.1%; Score 660; DB 7; Length 674;
Best Local Similarity 29.1%; Pred. No. 4.2e-45;
Matches 213; Conservative 141; Mismatches 262; Indels 116; Gaps 35;

QY 4 MSPYONKNEYEILS--SSNNTNPNRYPPAN--NRDMSTMWDCQGIS-----W 50
DB 1 MSP-NQNEYEIIIDATPSTVSNSNRYPFANEPTNALQNDYDKYDKLMSAGNASEYFGS 59

QY 51 DEIMESVETITSGINLIEFVIE----PSLGGINTLLS-IIGKLPTNRQTVSALSICDL 105
DB 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGPVLSVLTQILDILWPSGKESQWEIFMEQV 119

QY 106 LSIIRKEVADSVLSDAIDFDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIGQLVYVF 165
DB 120 BELINQKIAEYARNKALSLEGLGNVY-QLYLTALKEEENPNRFRSRQALRDVNRNF 178

QY 166 KLSERDFNEILGSLSRNNAOVLLPTFAQANVOLLLRDVAQVKAOWFPFLSAENVR 225
DB 179 EILDSLFQYM-PSFRTVNFVFPFLTVYAMAANLHLLKASIFGEW----- 226

QY 226 ELISPNSGCDFT--GDYVERLKCKTAETNYCLYVYQVGLNQIKOGGTGADTWSKFNKFR 283
DB 227 -----GWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKL--GTSAKQWVDYNQFR 277

QY 284 REMTLAVLDIIAIFPTDYDEKPLPHTVELTREIYTDVAG--YSGTYSWLRNWPNTNG 341
DB 278 REMTLAVLDVALLFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYDKAP-SFGV 336

QY 342 LEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVGTR-HYEDYTKNGIFQMSGTT 396
DB 337 IESSVIRPPHVDYITGLTVYQSRISISSARIYRWAGHQISYHRVSRGSL--QOMYGTN 395

QY 397 SN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVRGPDLYNDA 452
DB 396 QNLHSTSTFTDNYDIYKLSKDAVLLDIV-----YPGY-----TYIFPGMEVEFFMVN 445

QY 453 -----NGLSRMTIESTF-----PLVLHNSGVGRGSHRLSNAACV-VYGNR- 492
DB 446 QLNTRKTLKYNPVSVDIIASTRDSLELPETSDQPNYESYSHRLCHITSPATGNTTG 505

QY 493 -VNVYGVWTHSLKRENIIEANOITQIPAVKSYLQNYLANAYTVIKGT-HTGGDLIRPL 550
DB 506 LVPFVSWTHRSADLNTIYSDKITQIPAVKWC--DNL-----PFPVVKPGHGTGGDLQYN 560

QY 551 RTKSEYNVY-AGGGIRLIINNKTAGQSYRIRFRYAADKAAFFSVLYPGGWSNRVSL 609
DB 561 RSTGSGVTGLFARYGLAL---EKAGK-YRVLRYATDADIVLHV-----NDAQIQM 607

QY 610 EKSYSNYDDLVKSDPKFAEITPPLPSN-----TOMVEMOANSFQSDVNVVLKIEPL 665
DB 608 PKTMNFG-BDLTSKTPKVAADAITVNLATDSSVAVKHNVGDPNLSLGI-VYVDRIEPI 665

QY 666 PSNTTLEVEGE 677
DB 666 PVDET---YEAE 674

RESULT 12
US-11-108-389-44
; Sequence 44, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad

; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-44

Query Match 18.1%; Score 660; DB 7; Length 674;
Best Local Similarity 29.1%; Pred. No. 4.2e-45;
Matches 213; Conservative 141; Mismatches 262; Indels 116; Gaps 35;

QY 4 MSPYONKNEYEILS--SSNNTNPNRYPPAN--NRDMSTMWDCQGIS-----W 50
DB 1 MSP-NQNEYEIIIDATPSTVSNSNRYPFANEPTNALQNDYDKYDKLMSAGNASEYFGS 59

QY 51 DEIMESVETITSGINLIEFVIE----PSLGGINTLLS-IIGKLPTNRQTVSALSICDL 105
DB 60 PEVLVSGQDAAKAADIIVGKLLSGLGVFPVGPVLSVLTQILDILWPSGKESQWEIFMEQV 119

QY 106 LSIIRKEVADSVLSDAIDFDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIGQLVYVF 165
DB 120 BELINQKIAEYARNKALSLEGLGNVY-QLYLTALKEEENPNRFRSRQALRDVNRNF 178

QY 166 KLSERDFNEILGSLSRNNAOVLLPTFAQANVOLLLRDVAQVKAOWFPFLSAENVR 225
DB 179 EILDSLFQYM-PSFRTVNFVFPFLTVYAMAANLHLLKASIFGEW----- 226

QY 226 ELISPNSGCDFT--GDYVERLKCKTAETNYCLYVYQVGLNQIKOGGTGADTWSKFNKFR 283
DB 227 -----GWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKL--GTSAKQWVDYNQFR 277

QY 284 REMTLAVLDIIAIFPTDYDEKPLPHTVELTREIYTDVAG--YSGTYSWLRNWPNTNG 341
DB 278 REMTLAVLDVALLFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYDKAP-SFGV 336

QY 342 LEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVGTR-HYEDYTKNGIFQMSGTT 396
DB 337 IESSVIRPPHVDYITGLTVYQSRISISSARIYRWAGHQISYHRVSRGSL--QOMYGTN 395

QY 397 SN--DLRNIQFQADVYKITS--LAIMNLVGETTARPEYRVSKADFRVRGPDLYNDA 452
DB 396 QNLHSTSTFTDNYDIYKLSKDAVLLDIV-----YPGY-----TYIFPGMEVEFFMVN 445

QY 453 -----NGLSRMTIESTF-----PLVLHNSGVGRGSHRLSNAACV-VYGNR- 492
DB 446 QLNTRKTLKYNPVSVDIIASTRDSLELPETSDQPNYESYSHRLCHITSPATGNTTG 505

QY 493 -VNVYGVWTHSLKRENIIEANOITQIPAVKSYLQNYLANAYTVIKGT-HTGGDLIRPL 550
DB 506 LVPFVSWTHRSADLNTIYSDKITQIPAVKWC--DNL-----PFPVVKPGHGTGGDLQYN 560

QY 551 RTKSEYNVY-AGGGIRLIINNKTAGQSYRIRFRYAADKAAFFSVLYPGGWSNRVSL 609
DB 561 RSTGSGVTGLFARYGLAL---EKAGK-YRVLRYATDADIVLHV-----NDAQIQM 607

QY 610 EKSYSNYDDLVKSDPKFAEITPPLPSN-----TOMVEMOANSFQSDVNVVLKIEPL 665
DB 608 PKTMNFG-BDLTSKTPKVAADAITVNLATDSSVAVKHNVGDPNLSLGI-VYVDRIEPI 665

QY 666 PSNTTLEVEGE 677
DB 666 PVDET---YEAE 674


```
US-11-058-727-46
; Sequence 46, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-46

Query Match      18.1%; Score 660.5; DB 7; Length 675;
Best Local Similarity 29.1%; Pred. No. 3.8e-45;
Matches 216; Conservative 138; Mismatches 254; Indels 133; Gaps 37;

QY 4 MSPYQNKNEYILES--SSNNTNTPNRYPFAN--NRDMSTMSWDCQGIS-----W 50
DB 1 MSP--NNQNEYIIDATPSTSVSDNSRYPFANEPTNALQNDYKDYKMSAGNASEYPGS 59
QY 51 DEIWSEVETITSGINLIEFVIE-----PSLGGINTLLS--IIGKLIPTRQTVSALSICDL 105
DB 60 PEVLVSGQDAKAAADIVGKLLSGLVGPFVGVISVLTQLIDILWPSEKESQWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIDFCKLKNRYEYLSYLGAWLKD-----GKPLQKTNNS 156
DB 120 BELINQKIAEYARNKALSEGLEGNYY--QLYLTALEEWEENPNRSRFRGPAALRDVNR 178
QY 157 DIGQLVYFKLSERDFNEILGSLSRNNAQVLLLPFAQAAANVQLLLRDADVQYKAQWFP 216
DB 179 -----FEILDSLFTQYM--PSFRVTNFEVPLTVYAMAANLHLLLKXASIFGEW-- 227
QY 217 FLAENVRSELISPNSCDFT--GDYERLCKTAEYTNCLYTYQVGLNQIKOGGTGAD 274
DB 228 -----GWSTTTINNYDRQMKLTAEYSDHCVKVETGLAKLK--GTSAK 269

QY 275 TWSKENKFEREMTLAVLDIIAIFPTVDEKPLPHVLTREIYTDVAG--YSSGTYSWL 332
DB 270 QWVDYNOQFREMFLAVLDVFPNPDYTRTPMETKAQLTREYVTDPLGANNVSGISGY 329
QY 333 RNWPNTFNGLEANGTRGPGVLTWLSKIGIYNYEVS-----RYFAGVWGR--HYEDYTKNG 387
DB 330 DKAP--SFGVIESVIRPPHVDYITGLTYTOSRISISSARYTHWAGHQISVHRYSRGSN 388
QY 388 IFQMSGTTSN--DLRNIQFQADVYKITS--LAINLVGETTARPEYRVSKADPRRVGG 443
DB 389 L--QOMYGTQNQLHSTFTDFTNYDIYKTLSDKAVLLDIV-----YPGY-----TVIFFGM 437
QY 444 PDLNYDAGN-----NGLSRWTIESTF-----PLVHNSGVNGRPSHRLSNAAC 485
DB 438 PEVEFFMWNQNLNTRKTLKYNPVSKDITIASTRDSELELPDTPETSQPNYESYHRLCHITS 497
QY 486 V-VYGNRSR--VNVYGWTHTSLKRENIIEANQITQIPAVKSYYLQNLANAYTVIKGT-H 541
```

```
US-11-108-389-46
; Sequence 46, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-46

Query Match      18.1%; Score 660.5; DB 7; Length 675;
Best Local Similarity 29.1%; Pred. No. 3.8e-45;
Matches 216; Conservative 138; Mismatches 254; Indels 133; Gaps 37;

QY 4 MSPYQNKNEYILES--SSNNTNTPNRYPFAN--NRDMSTMSWDCQGIS-----W 50
DB 1 MSP--NNQNEYIIDATPSTSVSDNSRYPFANEPTNALQNDYKDYKMSAGNASEYPGS 59
QY 51 DEIWSEVETITSGINLIEFVIE-----PSLGGINTLLS--IIGKLIPTRQTVSALSICDL 105
DB 60 PEVLVSGQDAKAAADIVGKLLSGLVGPFVGVISVLTQLIDILWPSEKESQWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIDFCKLKNRYEYLSYLGAWLKD-----GKPLQKTNNS 156
DB 120 BELINQKIAEYARNKALSEGLEGNYY--QLYLTALEEWEENPNRSRFRGPAALRDVNR 178
QY 157 DIGQLVYFKLSERDFNEILGSLSRNNAQVLLLPFAQAAANVQLLLRDADVQYKAQWFP 216
DB 179 -----FEILDSLFTQYM--PSFRVTNFEVPLTVYAMAANLHLLLKXASIFGEW-- 227
QY 217 FLAENVRSELISPNSCDFT--GDYERLCKTAEYTNCLYTYQVGLNQIKOGGTGAD 274
DB 228 -----GWSTTTINNYDRQMKLTAEYSDHCVKVETGLAKLK--GTSAK 269
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Matches	216;	Conservative	136;	Mismatches	252;	Indels	135;	Gaps	38;
Qy	4	MSPYQKNEYETLES--SSNNTNTNRRYPFAN--NRDMSTWSWDCQGIS-----W	50						
Db	1	MSP--NNQNEYELIDATPSTSVSNDNRYPFANEPTNALQNMDYKDYLKMSAGNASEYPGS	59						
Qy	51	DEIWESVETITSIGINLIEFVIE-----PSLGAGINTLLS-IIGKLPIPTNRQTSVLSICDL	105						
Db	60	PEVLVSGDGAAKAADIIVGKLLSGLVGVPFVGPVLSVLTQLDILWPSEKSKQWEIFMEQV	119						
Qy	106	LSIIRKEVADSVLSDAIDAFQGLKKNYREYLSYLGAWLKD--GKPLQKTNNSDIGOLV	162						
Db	120	BELINQKIAEYARNKALSEGLEGNVY-QLYLTALEEWENPNRSRALRDVNRN-----	172						
Qy	163	YFVKLSERDFNEILGGSLSRNNQVLLPTFAQAAANVOLLRLLRADAVQYKAQWFFPLSAEN	222						
Db	173	--FEILDSLFTQYM--PSPRVNTNFVEPFLTIVYAMAANLHLLLLKDAISFGEEW-----	221						
Qy	223	VRSELISPNSCDDFT--GDYERLCKTAETVNTNCLVYWGVLNQIKOGGTGADTWSPFN	280						
Db	222	-----GWSTTTINNYDROKULTAEDSDHCVRWYETGLAKLK--GFSAKQWVDYN	269						
Qy	281	KFRREMTLAVLDIIDAIFPTDFEKPFLPTHVELTREIYTDVAG--YSGTYSWLRNWPNT	338						
Db	270	QFREMTLAVLDVVALFENYDTRIYPMETKAQLTREVIYTDPLGAVNVSSIGSWYDKAP-S	328						
Qy	339	PNGLAENGTRGPGGLVTWLSKIGIYNEVVS-----RYFAGWVGTR-HYEDYTKNGIGIFORMS	393						
Db	329	FGVIESSVIRPPHVPDYITGLTVYTSQSSISSARYIRHWAGHQISYHRVSRGSLN-QQMY	387						
Qy	394	GTTSN--DLRNIQFQNAVYKITS--LAIMNLVGETTARPYRVSVKADFRRVGGPDNLND	449						
Db	388	GTNQNLHSTSTFDTNVDIYKTLSDAVLLDIV-----YPCY-----TYIPFGMEVEFF	437						
Qy	450	AGN-----NGLSRMTIETFF-----PLVLHSGVVRGSPSHRLSNAACV-VIGN	490						
Db	438	MVNQLNNTKRTLKYNPVSKDIIASTRDSLELPPETSDQPNYESYSHRLCHITSIPATGN	497						
Qy	491	SR--VNVVWGWHTSLKRENIIEANQITQIPAVKSYLYONLYANAYTVVIGT-HTGGDLI	547						
Db	498	TTGLVVPFWSVTHRSADLNNTIYSDKITQIPAVKCN--DNL---PFVPVVKPGPHTGDBLL	552						
Qy	548	RFLTKSEYNNAVY-AGGGIRLIINNKTAGOSYRIRFRYAADKAAPFFSVILYPGGWGSNRF	606						
Db	553	QYNRESTGCVGLFLARYGLAL-----EKAGK-YRVRLRYATDADIVLHV-----	599						
Qy	607	VSLEKSYSGNYDDLUKYSDFKPAEIIITPLPSSNIQMDVEM-----QANSFQSDYVVV	658						
Db	600	IQPKTWNPG-EDLTSKTFKVADAIT---TLNLTATDSSIALKHNLEDPNSTLSGI-VY	653						
Qy	659	LDKIEFLPSSNTTILEYGE	677						
Db	654	VDRIEFTPVDET---	669						

RESULT 7

```

RESUL /
; Sequence 12, Application US/1108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Prenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/1

```

```

; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 669
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis (truncated)
US-11-108-389-12

Query Match      18.1%; Score 660.5; DB 7; Length 669;
Best Local Similarity 29.2%; Pred. No. 3.8e-45;
Matches 216; Conservative 136; Mismatches 252; Indels 135; Gaps 38;

Qy      4 MSPYQNKVEYIEILLES--SSNNTTNPKNYPAN--NRDMSTMSWDCQGIS-----W 50
Db      1 MSP--NQNEVEIIDATPSTSVSDNSNRYFPANETNALQNMWDKYDLKWSAGNASEYPGS 59

Qy      51 DETWSEVETITSGINLIEFVIE-----PSLGGINTLLS--IIGKLIPTNQTTVSALSICDL 105
Db      60 PEVLVSQDAAKAAIDIVGKLLSGLGVFPFVGPVTSVLTQLIDILWPSGSEKSWEIFMEQV 119

Qy      106 LSIIRKEVADSVLSDAIADPDGKLKNRYEYLSYLGAWLKD--GKPLQKTNNSDIGQLV 162
Db      120 EELINKKIAIYARKKALSELEGUNNY--QYLTLALBEEBENPNGSRALRDVNR----- 172

Qy      163 YPFKLSERDFNEILGGSLSRNAQVLLLPTFAQAAVQLLLLRDAVQYKAQWPPFLSAEN 222
Db      173 --FEILDSLFTQY--PSFRVTFNFEVPLTVYAMAANLHLLLKDAISIFGEW----- 221

Qy      223 VRSELISPNSGCDFT--GDYERLCKTAETNYCLYTYQVGLNQIKQSGTGADTWSKFN 280
Db      222 -----GWSTTTINNYDRQMKLTAEYSDHCVKVYETGLAKLK--GTSAKQWVDYN 269

Qy      281 KPRREMTLAVLDIIAIFPPYDEKYPPLPHVELTREIYTDVAG--YSSGTYSWLRNWPNT 338
Db      270 QFRREMTLAVLDVVVALLFPNDDTQYEMETKAQUTREVYTDPLGAVNVVSGISGYDKAP-S 328

Qy      339 FNGLEANGTRGPGVLVTLWSKIGIYNEVVS-----RYFAGWVGTR--HYEDYTKGNIGIFQ RMS 393
Db      329 FGVIESSVIRPPHVFYDITGLTVYTSQRSISSARYIRHWAGHQISYHRVSRGSNL--QQMY 387

Qy      394 GTTSEN--DLRNIDFQADVYKITS--LAINLVGETTARPEYRVSKADFRFRVGGPDLNVD 449
Db      388 GTQNQLHSTSTPFDFTNYDIYKTLSDKDAVLDDIV-----YPGY-----TYIFFGMPEVEFF 437

Qy      450 AGN-----NGLSRWMTIESTE-----PLVLHSGVGRGSPSHLSNAACV--VYGN 490
Db      438 MVNQLNTRKTLKYNPVSKDIIATSTRDSLELPPETSDQPNVESYSHRLCHITSIIPATGN 497

Qy      491 SR--VNVYGWHTSLKRENIIEANQITQIPAVKSYLYQLYLANAYTYVIKGT--HTGGDLI 547
Db      498 TTGLVVPVFSWTHRSADLNTIYSDKITQIPAVKCM--DNL-----PFVPVVKPGHGTGGDLL 552

Qy      548 RFLRTKSEYNAVY--AGGIRLLINNKTAQCSQRIIRFRYAADAARFVSYYLYPGGWSGNRF 606
Db      553 QYNRSTGSGVGLTFLARYGLAL-----EKAGK--YRVLRLRYATDADIVLHV-----NDAQ 599

Qy      607 VSLEKSYSGNYDDLKYSDFKFAEIIPTPLPSNIOQMDVEM-----QANSFQSDVNIV 658
Db      600 IQMPKTMNPG--EDLTSKTFKVADAIT-----TLNLTADSSIALKHNLDGPNSTLSGI--VY 653

Qy      659 LDKIEFLPSNTTTLEYEGE 677
Db      654 VDRIEFIPVDET---YEAE 669

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RESULT 8

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Db 438 MNQLNTRKTLKYNPVSKDIIASTRDSLELPETSDQPNYESYSHRLCHITSIPATGN 497
Qy 491 SR--VNVYGVWTHSTLKRNIIEANQITQIPAVKSYLYQNYLANAYTYVIKGT-HTGGDLI 547
Db 498 TTGLVPVFWSTHRSADLNNTIYSDKITQIPAVKCM--DNL---PFVVPVKGPGHGTGGDL 552
Qy 548 RFLRTKSEYNAVY-AGGGIRLIINNKTAGQSVRIIRPRYAADKAAFPSSVLYLPGGWSNRF 606
Db 553 QYNRSTGSGVTLFLARYGLAL-----EKAGK-TRVRLRYATDADIVLHV-----NDAQ 599
Qy 607 VLSKSYSGNYDDLYSDKFKFAEIIITPLPSSNIQMDVEM-----QANSFQSDVNVV 658
Db 600 IQPKTMNPG-EDLTSKTFKVADAIT-----TLNLATDSSLALKHNLGDPNSTLSGI-VY 653
Qy 659 LDKIEFLPSNTTILEYGE 677
Db 654 VDRIEFIPVDET---YEAE 669

RESULT 5
US-11-058-727-12
; Sequence 12, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-11-058-727-12

Query Match 18.1%; Score 660.5; DB 7; Length 669;
Best Local Similarity 29.2%; Pred. No. 3.8e-45;
Matches 216; Conservative 136; Mismatches 252; Indels 135; Gaps 38;

Qy 4 MSPYONKNEYEILES--SNNTNTNRYFPAN--NRDMSTMSWDCQIS-----W 50
Db 1 MSP-NNQNEYIIDATPSTSVSDNSRNPFPANPTNALQNMDDKYDKYKMSAGNASEYFGS 59
Qy 51 DRIMESVETITSIGINLIEFVIE---PSLGGINTLLS-IICKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAKAAADIVKLSGLGVFPVGVFVLSYLTQILDLNPSGEKSWEIFMGOV 119
Qy 106 LSIRKEVADVLSDAIDFDGKLNRYEYLSYGWLKD---GKPLQKTNNSDIGQLV 162
Db 120 EELINQKIAEYARNKALSLEGLGNNY-QLYLTALTEEWENPNNGSRALRDVNR----- 172
Qy 163 YVEKLSERDFNIELGSLSRNNAQVLLLPFAQANVOLLILRDVQYKQWFPFLSABN 222
Db 173 --FEILDSLFTQYM-PSFRVTFVFPFLLTVYAMAANLHLLKDKASIFGEW----- 221
Qy 223 VRSELISPNSGCDFT--GDYERLCKTAETNYCLYQVGLNQLKQGGTGADTWSKFN 280
```

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Db 222 -----GWSTTTINNYDROKMLTAESYDHCVRKYETGLAKLK--GTSAKOMVDYN 269
Qy 281 KFRREMTLAVLDIIAIFPTYPEKYPLPHTHVELTREIYTDVAG--YSSGTYISWLRNWPNT 338
Db 270 QFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVVSSIGSWYDKAP-S 328
Qy 339 FNGLEANGTRCPGLVTLWSKIGIYNEYVS-----RYFAGVWGR-HYEDYTKNGNIGIFORMS 393
Db 329 FGVIESSVIRPHVPFDYITGLTVYTQSRSSISSARYIRHWAGHOISYHRVSRGSLN-QQMY 387
Qy 394 GTTNS--DLRNIIDFONADVYKITS--LAIMNLVGETTARPEYRVSKADPRRVGGPDLDVND 449
Db 388 GTNQLHSTSTFDFNYDIYKTLKDAVLLDIV-----YPGY-----TYIFFGMEVEFF 437
Qy 450 AGN-----NGLSRMTIESTF-----PLVLHNSGVGRGFSHRLSNAACV-VYGN 490
Db 438 MNQLNTRKTLKYNPVSKDIIASTRDSLELPETSDQPNYESYSHRLCHITSIPATGN 497
Qy 491 SR--VNVYGVWTHSTLKRNIIEANQITQIPAVKSYLYQNYLANAYTYVIKGT-HTGGDLI 547
Db 498 TTGLVPVFWSTHRSADLNNTIYSDKITQIPAVKCM--DNL---PFVVPVKGPGHGTGGDL 552
Qy 548 RFLRTKSEYNAVY-AGGGIRLIINNKTAGQSVRIIRPRYAADKAAFPSSVLYLPGGWSNRF 606
Db 553 QYNRSTGSGVTLFLARYGLAL-----EKAGK-TRVRLRYATDADIVLHV-----NDAQ 599
Qy 607 VLSKSYSGNYDDLYSDKFKFAEIIITPLPSSNIQMDVEM-----QANSFQSDVNVV 658
Db 600 IQPKTMNPG-EDLTSKTFKVADAIT-----TLNLATDSSLALKHNLGDPNSTLSGI-VY 653
Qy 659 LDKIEFLPSNTTILEYGE 677
Db 654 VDRIEFIPVDET---YEAE 669

RESULT 6
US-11-108-389-6
; Sequence 6, Application US/1108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Maize optimized Cry1218-1
US-11-108-389-6

Query Match 18.1%; Score 660.5; DB 7; Length 669;
Best Local Similarity 29.2%; Pred. No. 3.8e-45;
```

```
; TITLE OF INVENTION: poynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 4
; LENGTH: 1316
; TYPE: PRT
; ORGANISM: Bacillus popilliae
US-11-091-643-4

Query Match      18.3%; Score 668; DB 7; Length 1316;
Best Local Similarity 31.1%; Pred. No. 2.5e-45;
Matches 232; Conservative 105; Mismatches 262; Indels 148; Gaps 35;

QY      8 QNKNEYEILESSNN-TNTNPNRYPPANRDM-----STMSWND-CQG-----IS 49
Db      33 QSGNEMQIIQPSSNALLYSPNKYPATDPNVIAEGGSYKNWLDCTGTGTRSPETAAS 92
QY      50 WDEIWESVETITSGINLIEFVIEPSLGGINTILLISIIIGKLIPNRTQTVSALSICDLSII 109
Db      93 KGAVSAAI-TISGLIGLGLGVPPFASQIGAPYTFL--LNTLWPAS-NTQWEQFIAHVEELI 148
QY      110 RKEVADSVLSDAIDPDGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGQLVYYPKLS 169
Db      149 NAKLTDHVRNSALTKLNG-LRNNIEIYNEALIVWKD-----PNNS-----KLKD 192
QY      170 RDNFEILG-----GSLSRNNAQVLLPTFAQAANVOLLRLRDAVQYKAQW-FPFLS 219
Db      193 DVRSKFVGLNSQPEEYIPQKEGFEVQLLTIYAQSANLHLLLRDSSLYGASWGFAQAT 252
QY      220 AENVRSSELSPNSGCDFTGDYERLCKTAETNYCLYQVGLNQIKOGGTGADTWSP 279
Db      253 IDN-----NYNRQIRKTAEYANHCCTTWTYQGLQRLQ--GTTASSWLSY 293
QY      280 NKFRREMTLAVLDIIAIFPTYDPEKYPLPHTVELTREIYTDVAGYSSGTYSLRNWPNTP 339
Db      294 HRFREMTLVLIDICALFSYNDARSYPLEVRGELTREIYTDVP--APGT-NMIDRAP-SF 349
QY      340 NGLANGTRGPGVLTWLSKIGIYNEYSVRYFAGWGTG-----HYEDYTKNGIGIFORMSG 394
Db      350 AEIENLVIRAPRTVTWIS--GDLIVYTGRLY-GYTGNNDYAAHRLDFLETNG--YRPEG 404
QY      395 TTSNDRLNID-----FQNAVYKITSLAIMN-----LVGETTARPEYRVSKADFRV 441
Db      405 PTYGSTINISRTDSIPMNSIDYVSTTVTVGSAMPTGGFVLGVASAR-----FFSKS 456
QY      442 GGPDLNVDAGNGLSRMTIESTPLVLHNGV-----RGPSHRLSNAACVYVG-NSRV 493
Db      457 PSTGL---LGERVYQNPVFSSTLTFLNPGVDQDPTTAADYSHKLSCTAPRTGLNGTV 513
QY      494 NVYGMWHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVYIKGT-HTGDLIRFLRT 552
Db      514 PVFGYRSATVSRNRIEIPDKITQIPAVKSNLDN-----CPVVRGTGFTGCDWL----- 562
QY      553 KSEYNAYAGGGRILINNKTKAQSYRIRFRAADKAAFFSVLYPGGWGNSN-----RPV 607
Db      563 KTSYLSVVF-----LFTISSRAGQSYRIRVYAAAVDLIMSIV-----SNDPFIISKGI 610
QY      608 SLEKSYSGNYDDLKYSDKFAET-ITPPLPSSNIQMDVEMQANSFOSDVNVVLDKTEFLP 666
Db      611 SLTKSMPPLETVPYEAFAFADPGVITTTATANKRTTFO-----FHTGGAALIIDRIEFVP 665
QY      667 SNTTILEYGERDLEKTKNAVNDLFTN 693
Db      666 IEGSLPEYETKQLEKAKAVNHLFTD 692
```

RESULT 4

```
US-11-058-727-6
; Sequence 6, Application US/11058727
; Publication NO. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Maize optimized Cry12Ib-1
US-11-058-727-6
```

Query Match 18.1%; Score 660.5; DB 7; Length 669;

Best Local Similarity 29.2%; Pred. No. 3.8e-45;

Matches 216; Conservative 136; Mismatches 252; Indels 135; Gaps 38;

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QY      4 MSPYQNKNEYEILES--SSNNNTNPNRYPPAN--NRDMSTMSWND-CQGIS-----W 50
Db      1 MSP--NNQNEYELIIDATPSTSVNSDSNRYPFANPTNALQNDYKYLKMSAGNASEYPOS 59
QY      51 DEIWESVETITSGINLIEFVIE-----PSLGGINTLLS-IIGKLIPNRTQTVSALSICDL 105
Db      60 PEVLVSGQDAAKAADIVGKLLSGLGVFPVGPVIVSLYQLIDILWPSGSKSQWEIFMEQV 119
QY      106 LSIIRKEVADSVLSDAIDPDGKLNRYEYLSYLGAWLKD---CKPLOKTNNSDIGQLV 162
Db      120 BELINQKIATYARNKALSELEGLGNVY-QLYLTALBEEBENPNNGSRALRDVRNR----- 172
QY      163 YVFKLSERDFNEILGGSLSRNNAQVLLPTFAQAANVOLLRLRDAVQYKAQWFPFLSAEN 222
Db      173 --FEILDSLFTQYM-PSFRVTNFEVPLTVVYMAANLHLLLLKDAISIFGEW----- 221
QY      223 VRSELISPSNGCDFT--GDYYERLCKTAETNYCLYQVGLNQIKOGGTGADTWSPKN 280
Db      222 -----GWSSTTINNYDROMKLTAEYSDHCVKVVETGLAKLK--GTSAKQWVDVN 269
QY      281 KFRREMTLAVLDIIAIFPTYDPEKYPLPHTVELTREIYTDVAG--YSSGTYSLRNWPNTP 338
Db      270 QFRREMTLAVLDVVALFPNYDTRTPYMETKAQLTREVTYDPLGAVNVVSSIGSWYDKAP-S 328
QY      339 FNGLEANTRGPGVLTWLSKIGIYNEYVS---RYFAGWVGTR-HYEDYTKNGIGIFORMS 393
Db      329 FGVTESSVIRPHVPDYITGLTVYTSQSRSSISARVIRHWAGHOISYHRVSRGSLN-QQMY 387
QY      394 GTTGN--DLRNIIDFONADVYKITS--LAIMNLVGETTARPEYRVSKADFRRVGGPDLNVD 449
Db      388 GTNQNLHSTSTFDFTNYDIYKTLSDKAVLLDIV-----YPGY-----TVIFPGMPEVEBF 437
QY      450 AGN-----NGLSRMTIESTF-----PLVLSHNGVRGSPSHLSNAACV-VYGN 490
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```

QY 163 YFKLSERDFNEILGSLSRNNAOVLLPTFAQANVOLLILLRDAVOYKAOQWFPFLSAEN 222
Db 173 --FEILDSLFTQYM-PSFRVTNFEVFPFLTVYAMAANLHLLLLKDAIFGEW-----221
QY 223 VRSELISPNSGCDF--GDYERLCKTAETNYCLYQVGLNQIKOGGTGADTWSKFN 280
Db 222 -----GWSTTTINNYDRQMKLTAEYSDCHVKWYETGLAKL-K-GTSAKQWVDYN 269
QY 281 KFRREMTLAVLDIIAIPPTDYDEKYPPLTHVELTREIYTDVAG--YSGTYSWLNRWPN 338
Db 270 QFRREMTLAVLDVALLFPNDYTRTPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAP-S 328
QY 339 ENGLEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVCTR-HYEDYTKNGIFORMS 393
Db 329 FGVISSVIRPPHVDIITGLTVYQSRSSISSARIYRWAGHQISYHRVSRGSNL-QQMY 387
QY 394 GTTSN--DLRNIQADNADYKITS--LAIMNLVGETTARPEYRVSKADFRVGGPDLNVD 449
Db 388 GTNQLHSTSTFTDNYDIYKLSKDAVLLDIV-----YPGY-----TYIFFGMEVEVFF 437
QY 450 AGN-----NGLSRMTIESTF-----PLVLHNSGVRGSPSHRLSNAACV-VYGN 490
Db 438 MVNQLNTRKTLKYNPVSXKDIIASTRSELELPETSDQPNYESYSHRLCHITSIPATGN 497
QY 491 SR--VNVYGVWTHSLKRENIIEANQITQIPAVKSYLQNYLANAVYVIKGT-HTGGDLI 547
Db 498 TTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWC--DNL---PFVPVVGKPGHTGGDL 552
QY 548 RFLRTKSEYNNAV-AGGGIRLIINNKTAGOSYRIRFRAADKAAFFSVLYPGWGSNRF 606
Db 553 QYNRSTGSGVGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQ 599
QY 607 VLSKYSYGNVDDLYSDPKFAEITPPLPSSNIQMDVEM-----QANSFQSDVNVV 658
Db 600 IQMPKTNMGP-EDLTSKTFKVADAIT---TLNLATDSSLALKHNLDGDPNSTLSGI-VY 653
QY 659 LDKIEFLPSNTTLEVEGERDLEKTKNAVNDLFTN 693
Db 654 VDRIEFIPVDET---YEAQDLEAAKKAVALFTN 685

```

RESULT 2

```

US-11-108-389-2
; Sequence 2, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: Activity
; FILE REFERENCE: 357118/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis

```

US-11-108-389-2

```

Query Match 19.5%; Score 713.5; DB 7; Length 1206;
Best Local Similarity 30.1%; Pred. No. 5.3e-49;
Matches 227; Conservative 137; Mismatches 256; Indels 135; Gaps 38;
QY 4 MSPYONKNEVIELS--SSNNTNTPNRYPPAN--NRDMSTMSWDCQGIS-----W 50
Db 1 MSP--NNQNEVEIIDATSTSVSDNSNRYPPANFETNALQNDYDKLQMSAGNASEYPGS 59
QY 51 DEIWESVETITISIGINLIEFVIE----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
Db 60 PEVLVSGQDAKAADIIVGKLLSLGLGVFPVSVLTQLDILWPSGEKQWEIFMEQV 119
QY 106 LSITRKEVADSVLSADATADFGKLNRYREYLSYLGAWLKD---GKPLQKTNNGSDIGOLV 162
Db 120 EELINQIAEYARNKALSELEGLGNNY-QLVLTAALEEENPNRSRALRDYRNR-----172
QY 163 YFVKLSERDFNEILGSLSRNNAOVLLPTFAQANVOLLILLRDAVOYKAOQWFPFLSAEN 222
Db 173 --FEILDSLFTQYM-PSFRVTNFEVFPFLTVYAMAANLHLLLLKDAIFGEW-----221
QY 223 VRSELISPNSGCDF--GDYERLCKTAETNYCLYQVGLNQIKOGGTGADTWSKFN 280
Db 222 -----GWSTTTINNYDRQMKLTAEYSDCHVKWYETGLAKL-K-GTSAKQWVDYN 269
QY 281 KFRREMTLAVLDIIAIPPTDYDEKYPPLTHVELTREIYTDVAG--YSGTYSWLNRWPN 338
Db 270 QFRREMTLAVLDVALLFPNDYTRTPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAP-S 328
QY 339 ENGLEANGTRGPGVLTWLSKIGIYNEVVS---RYFAGWVCTR-HYEDYTKNGIFORMS 393
Db 329 FGVISSVIRPPHVDIITGLTVYQSRSSISSARIYRWAGHQISYHRVSRGSNL-QQMY 387
QY 394 GTTSN--DLRNIQADNADYKITS--LAIMNLVGETTARPEYRVSKADFRVGGPDLNVD 449
Db 388 GTNQLHSTSTFTDNYDIYKLSKDAVLLDIV-----YPGY-----TYIFFGMEVEVFF 437
QY 450 AGN-----NGLSRMTIESTF-----PLVLHNSGVRGSPSHRLSNAACV-VYGN 490
Db 438 MVNQLNTRKTLKYNPVSXKDIIASTRSELELPETSDQPNYESYSHRLCHITSIPATGN 497
QY 491 SR--VNVYGVWTHSLKRENIIEANQITQIPAVKSYLQNYLANAVYVIKGT-HTGGDLI 547
Db 498 TTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWC--DNL---PFVPVVGKPGHTGGDL 552
QY 548 RFLRTKSEYNNAV-AGGGIRLIINNKTAGOSYRIRFRAADKAAFFSVLYPGWGSNRF 606
Db 553 QYNRSTGSGVGLFLARYGLAL-----EKAGK-YRVLRYATDADIVLHV-----NDAQ 599
QY 607 VLSKYSYGNVDDLYSDPKFAEITPPLPSSNIQMDVEM-----QANSFQSDVNVV 658
Db 600 IQMPKTNMGP-EDLTSKTFKVADAIT---TLNLATDSSLALKHNLDGDPNSTLSGI-VY 653
QY 659 LDKIEFLPSNTTLEVEGERDLEKTKNAVNDLFTN 693
Db 654 VDRIEFIPVDET---YEAQDLEAAKKAVALFTN 685

```

RESULT 3

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US-11-091-643-4
; Sequence 4, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; insecticidal effect on scarabaeidae insects and

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2005, 11:12:01 ; Search time 12 Seconds
(without alignments)
388.934 Million cell updates/sec

Title: US-10-781-979-3

Perfect score: 3655

Sequence: 1 MKQMSPYQNKNEYEILSSS.....YEGERLEKTKNAVNDLFTN 693

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51463 seqs, 6734788 residues

Total number of hits satisfying chosen parameters: 51463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713.5	19.5	1206	7	US-11-058-727-2
2	713.5	19.5	1206	7	US-11-058-727-2
3	668	18.3	1316	7	US-11-091-643-4
4	660.5	18.1	669	7	US-11-058-727-6
5	660.5	18.1	669	7	US-11-058-727-12
6	660.5	18.1	669	7	US-11-058-389-6
7	660.5	18.1	669	7	US-11-058-389-12
8	660.5	18.1	675	7	US-11-058-727-46
9	660.5	18.1	675	7	US-11-058-389-46
10	660	18.1	674	7	US-11-058-727-44
11	660	18.1	674	7	US-11-058-727-50
12	660	18.1	674	7	US-11-058-389-44
13	660	18.1	674	7	US-11-058-389-50
14	660	18.1	676	7	US-11-058-727-40
15	660	18.1	676	7	US-11-058-389-40
16	659.5	18.0	675	7	US-11-058-727-78
17	659.5	18.0	675	7	US-11-058-389-78
18	659	18.0	674	7	US-11-058-727-76
19	659	18.0	674	7	US-11-058-727-82
20	659	18.0	674	7	US-11-058-389-76
21	659	18.0	674	7	US-11-058-389-82
22	659	18.0	676	7	US-11-058-727-72
23	659	18.0	676	7	US-11-058-389-72
24	658.5	18.0	673	7	US-11-058-727-8
25	658.5	18.0	673	7	US-11-058-727-26

26	658.5	18.0	673	7	US-11-058-727-30	Sequence 30, Appl
27	658.5	18.0	673	7	US-11-058-727-34	Sequence 34, Appl
28	658.5	18.0	673	7	US-11-108-389-8	Sequence 8, Appl
29	658.5	18.0	673	7	US-11-108-389-26	Sequence 26, Appl
30	658.5	18.0	673	7	US-11-108-389-30	Sequence 30, Appl
31	658.5	18.0	673	7	US-11-108-389-34	Sequence 34, Appl
32	658.5	18.0	677	7	US-11-058-727-52	Sequence 52, Appl
33	658.5	18.0	677	7	US-11-108-389-52	Sequence 52, Appl
34	657.5	18.0	673	7	US-11-058-727-70	Sequence 70, Appl
35	657.5	18.0	673	7	US-11-108-389-70	Sequence 70, Appl
36	657.5	18.0	675	7	US-11-058-727-42	Sequence 42, Appl
37	657.5	18.0	675	7	US-11-058-727-48	Sequence 48, Appl
38	657.5	18.0	675	7	US-11-108-389-42	Sequence 42, Appl
39	657.5	18.0	675	7	US-11-108-389-48	Sequence 48, Appl
40	657.5	18.0	677	7	US-11-058-727-84	Sequence 84, Appl
41	657.5	18.0	677	7	US-11-108-389-84	Sequence 84, Appl
42	657.5	18.0	1210	7	US-11-058-727-4	Sequence 4, Appl
43	657.5	18.0	1210	7	US-11-108-389-4	Sequence 4, Appl
44	656.5	18.0	675	7	US-11-058-727-74	Sequence 74, Appl
45	656.5	18.0	675	7	US-11-058-727-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-11-058-727-2
; Sequence 2, Application US/11058727
; Publication NO. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2

Query Match	19.5%	Score 713.5;	DB 7;	Length 1206;
Best Local Similarity	30.1%	Pred. No. 5.3e-49;		
Matches 227;	Conservative 137;	Mismatches 256;	Indels 135;	Gaps 38;
QY	4	MSPYQNKNEYEILS--SSNNTNTNRYPPFAN--NRDMSTMSWNCQGIS-----W 50		
Db	1	MSP--NNQNEYIIDATPSTVSNSNRYPPFANEPTNALQNMDYKDYKMSAGNASEYPGS 59		
QY	51	DEWESVETITSIGNLIEFVIE----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105		
Db	60	PEVLVSGQDAKAAIDIVGKLLSGVGVPVGLVSLYLTQILDILWPSEKSOEIMEQV 119		
QY	106	LSIRKEVADSVLSDAIDFDGKLNRYEYLSYLGAWLKD---GKPLQKTNNSDIGQIV 162		
Db	120	EELNQKTAETVARNKALSEGLGNNY-QLYVITALEEENPNNGSRALRDVNR----- 172		

Db 650 IEFIPVPTTR---EAKEDLEAAKAVASLFT 677

Search completed: December 15, 2005, 11:24:05
Job time : 170 secs

QY 347 TRGRLVTLWLSKIGLYNEVSRVY-----FAGVCTRHVEDYT-KGNGIFORMSGT- 396
 Db 329 TDSPLVRLWGLDMTITYGADISYRTPSGDRIGVWYGNINAFYHTRTDVVMFRTGDTA 388
 QY 397 ----GNDLRNIDFQADYK--ITSIAIMNLV--ETTARPEYRVSKADFRVVGPDNLN 448
 Db 389 YEDPSTFISNILD--DIKLDLRAAVSTIOMDIT--FGVSSRRFPDIRGNQLY 442
 QY 449 DAGNGLSRMTTESTFPLVLHNG--VRGPHSL-----SNAACVYVGNRNVYVWTH 500
 Db 443 QS-NKYPSPSLPTITTFPGESSEGNANDYSHLLCDVKILQEDSSNICGRSLLSHAWTH 501
 QY 501 TSLKENIIEANQITQIPAVKSYLQNYLANAYTVIKGT-HTGGDLIRFLRTKSEYNV 559
 Db 502 ASLDRNTILPEITQIPAVTAIEUR-----GNSVAVAGPGSTGGDLV-----KMSYHSV 551
 QY 560 YAGGIRLIINNKTAGOSYRIRFRYAADKAAPF-----SVLYPGMGWGNRFVLSKSY 613
 Db 552 WS---PKVVCSEL---KNVRVIRYASHGNCQFLMKRWPGSTGVAPQWABH---NVQCTF 602
 QY 614 SGNYDDLKYSDFKFAEITTPPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
 Db 603 S---NSMRYEAPKYLDITFTEENNFAFTIDLESQG-----DLFIDKIEFIPVSGSAFE 654
 QY 674 YEGERDLEKTKAVNDLFTN 693
 Db 655 YEGKONIEKTKAVNDLFTN 674

RESULT 13

US-11-018-615-13
 ; Sequence 13, Application US/11018615
 ; Publication No. US20050138685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ronald D. Flannagan
 ; TITLE OF INVENTION: Bacillus Cry9 Family Members
 ; FILE REFERENCE: 035718/285985
 ; CURRENT FILING DATE: 2004-12-21
 ; PRIOR APPLICATION NUMBER: 60/531,807
 ; PRIOR FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 1151
 ; TYPE: PRT
 ; ORGANISM: Bacillus thuringiensis DSIR517
 US-11-018-615-13

Query Match 20.4%; Score 747; DB 6; Length 1151;
 Best Local Similarity 30.6%; Pred. No. 1.4e-50;
 Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;
 QY 9 NKNEVEILLESSNNTNTPN--RYPFANNRDMSTMSNDCQG---LSW-DEIWESEVETITS 62
 Db 2 NQNKGIIGASCGGASDDVAKYPLANNPYSSALNLSQNSIILNINIGDAAKEAVS 61
 QY 63 IGINLIEFVIEPSLGG--INTLSIIGKLI--PTNRQTVSALSICDLSIIRKEVADSVLSD 120
 Db 62 IGTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQISDLSICDLSIIDLRVSGVLND 121
 QY 121 ATADPDGKLKNRYEYLYVLGAWLKDGKPLQKTNNSDIGOLVYVFKLSERDFNEIL---- 176
 Db 122 GIADFNGLVLYRN--YLEALDSWNKN-----PNSASAEELRTPRIADSEFDRILRGS 174
 QY 177 ---GGSLRNNAQVLLLPTEFAANVQILLRLDVAQYKAQW-----FPLSAENVRSLEI 228
 Db 175 LTNGSLAKQNAQIILLFSFASAAFPHLLLLLDATRYGTNMGWLNATPFINYQSKLVELI 234
 QY 229 SPNSGCDFTGDYIERLCKTAYTNYCYLYWYVGLNQIKQGGTGADTWSKFNKPREMTL 288

Db 235 E-----LYTDYCVHVNVRGNELRQGTSAWLEFHRVREMTL 274
 QY 289 AVLDIILAIFFPYDEKYPPLPHTBELTRIYDVAVG-----SSGYSMRLR--NWPNTFNL 342
 Db 275 MVLDIVASFSSLDITNYPIETDFQLSRVITYDPIGFVHRSSLRGESWFSFVNRRAN--FSDL 333
 QY 343 EANGTRGPGLVTLWSKIGLYNEVSRVYFAG-----WVGTRHYEDYTKNGIIFORMSGT 395
 Db 334 E-NAIPNRPSPFWFLNNMIIISTGSLTLPVSPSTDRARVWYGSRRDRISPANSOFITELISGQ 392
 QY 396 TSNDRINIDFQADYKITSIAIMNLVGETTARPEYRVSKADFRVVGPDNLNIDAGNGL 455
 Db 393 HTTATQITLGN--IPVDSQA--CNL--NDIT--YGVNRAVF-----YHDASEGS 435
 QY 456 SRMTIESTFPLVLHNSGVGRP-----SHRLSNAACVYVVG----- 489
 Db 436 QRSVYEG---YIRTTGIDNPRVQINITYLPGENSIDPTPEDYTHILSTTINLTGLRQV 491
 QY 490 ---NSRVNVYVWTHSLKRENIIEANQITQIPAVKSYLQNYLANAYTVIKGTHTCGD 545
 Db 492 ASNRSSLVWYVWTHSLKRENIIEANQITQIPAVKSYLQNYLANAYTVIKGTHTCGD 547
 QY 546 LIRELRTKSEYNVYAGGIRLIINNKTAGOSYRIRFRYAADKAAPFVSVLYPGMGWGNR 605
 Db 548 LLQ-----RTDHGSL-----GVLRVQFPLHLRQYRIRVRYASTTIRLSV-----NGS 591
 QY 606 FVSLEKSYSGNY-----DDLKYSDFKFAEITTPPLP--SSNIQMDVEMQANSFQSDVNVVLDK 661
 Db 592 FGTISQNLPTMRLGEDLRYGSPFAIREFNTSIRPTASPDQIRLTIEPSFIRQEVV--DR 649
 QY 662 IEFLPSNTTILEYGERDLEKTKAVNDLFTN 692
 Db 650 IEFIPVNPTR---BAKDELEAKKAVASLFT 677

RESULT 14

US-10-099-285-70
 ; Sequence 70, Application US/10099285
 ; Publication No. US20030105319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schnepf, H. Ernest
 ; Narva, Kenneth E.
 ; Walz, Michelle
 ; Stockhoff, Brian
 ; Muller-Cohn, Judy
 ; TITLE OF INVENTION: Toxins Active Against Pests
 ; NUMBER OF SEQUENCES: 105
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 15-Mar-2002
 ; FILING DATE: 15-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION NUMBER: 09/002,285
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/886,615
 ; FILING DATE: 1-JUL-1997
 ; APPLICATION NUMBER: US 08/674,002
 ; FILING DATE: 1-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sanders, Jay M.

```
Db 552 WS---FKVYCSSEL---KNYVRIRYASHGNCQFLMKRWSTGVAPQWRAH---NVQGTG 602
QY 614 SGNVDDLYKSDPKFABIITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
Db 603 S---NSMRVEAFKYLDIFTITPEENNFAFTIDLESG-----DLFDKIEFIPVSGSAFE 654
QY 674 YEGERDLEKTKNAVNDLFTN 693
Db 655 YEGKQNIKTQKAVNDLFIN 674

RESULT 11
US-10-783-417-15
; Sequence 15, Application US/10783417
; Publication No. US20040216186A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-006, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274146
; CURRENT APPLICATION NUMBER: US/10783,417
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,806
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 674
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
US-10-783-417-15
```

```
Query Match 22.7%; Score 831; DB 5; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY 4 MSPYQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCOG--ISWDEIWE 55
Db 1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVMMKNGYKDWNECEGNSISPSAAA 60
QY 56 SVETITSGINLIEFIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVAD 115
Db 61 ITSQKIVSVLTKLAKAVASSLA--DSIKSSLGISKITITENNVSQVMQVQHOIINRRIQE 118
QY 116 SVLSDAIADFDGKLKNYREYLYSYLGAWLKDGKPLQKTNNSDIG---QLVYFVKLSERDF 172
Db 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKSNINYQTNVAAEFKTVVEREF 170
QY 173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVAVQYKAQWFPFLSAENVSELSISPS 232
Db 171 FTKLGIYRTSSQITLLPTTQAANLHLSMLRDVAVMQEGW-----NLQSHI----- 218
QY 233 GCDFTGDIYERLCKTAETNTYCLWYQVGLNQIKQGGTGADTWKSKFNKFRREMTLAVLD 292
Db 219 -----NYSKELDDALEDYTCVEYTKGLNALR--GSTAID-WLEFNSFRDMLTAVLD 270
QY 293 IIAIPTYDFEYKPLPPTHVELTREIYTDVAVGSSGTYSWLRNWPNT-----FNGLEANG 346
Db 271 LVAIFFPNVPYRPLSTKISLSRKIYTDVPVGRDTSPPS---FGDWTNTGRTLNFNDLREV 328
QY 347 TRGPGIATVLSKIGIYNEVVSRY-----FAGVVGTHYEDYT--KNGNIFORMSGTT- 396
Db 329 TDSPLSVKWLGMWTIYTGADISYRTPSPGDRIGVWYGNINAFHYHGRDVTVMFROQTGDTA 388
QY 397 ----SNDLRNIDFQNAVYK--ITSLAIMNLVG--ETTARPEYRVSKADFRVVGPGDNLN 448
Db 389 YEDPSTFISNILYD--DIYKLDRAAAVSTIQGAMDDT-----FGVSSSRFFDIRGNQLY 442
```

```
QY 449 DAGNGLSRMTIESTFPPLVLHSGN-VRGPSHRL-----SNAACVYVYGNRNVVYGVWTH 500
Db 443 QS-NKFPYPSLPITITPPGEESEGANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTH 501
QY 501 TSLKRENIIEANQITQIPAVKSYLQNYLANAVTVYIKGT-HTGGDLIRFLRTKSEYNAV 559
Db 502 ASLDRNNTLDPETITQIPAVTAYELR-----GNSSVVAGPGSTGGOLV-----KMSYHSV 551
QY 560 YAGGGIRLIINNKTAGQSYRIRFYAADAKAFF-----SVLYPGGWSGNRNVFSLEKSY 613
Db 552 WS---FKVYCSSEL---KNYVRIRYASHGNCQFLMKRWSTGVAPQWRAH---NVQGTG 602
QY 614 SGNVDDLYKSDPKFABIITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
Db 603 S---NSMRVEAFKYLDIFTITPEENNFAFTIDLESG-----DLFDKIEFIPVSGSAFE 654
QY 674 YEGERDLEKTKNAVNDLFTN 693
Db 655 YEGKQNIKTQKAVNDLFIN 674

RESULT 12
US-10-781-979-22
; Sequence 22, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 674
; TYPE: PRN
; ORGANISM: Bacillus thuringiensis
US-10-781-979-22
```

```
Query Match 22.7%; Score 831; DB 5; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY 4 MSPYQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCOG--ISWDEIWE 55
Db 1 MNQYQNKNEYEILESSQNNMNNPNRYPPADDPNAVMMKNGYKDWNECEGNSISPSAAA 60
QY 56 SVETITSGINLIEFIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVAD 115
Db 61 ITSQKIVSVLTKLAKAVASSLA--DSIKSSLGISKITITENNVSQVMQVQHOIINRRIQE 118
QY 116 SVLSDAIADFDGKLKNYREYLYSYLGAWLKDGKPLQKTNNSDIG---QLVYFVKLSERDF 172
Db 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKSNINYQTNVAAEFKTVVEREF 170
QY 173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVAVQYKAQWFPFLSAENVSELSISPS 232
Db 171 FTKLGIYRTSSQITLLPTTQAANLHLSMLRDVAVMQEGW-----NLQSHI----- 218
QY 233 GCDFTGDIYERLCKTAETNTYCLWYQVGLNQIKQGGTGADTWKSKFNKFRREMTLAVLD 292
Db 219 -----NYSKELDDALEDYTCVEYTKGLNALR--GSTAID-WLEFNSFRDMLTAVLD 270
QY 293 IIAIPTYDFEYKPLPPTHVELTREIYTDVAVGSSGTYSWLRNWPNT-----FNGLEANG 346
Db 271 LVAIFFPNVPYRPLSTKISLSRKIYTDVPVGRDTSPPS---FGDWTNTGRTLNFNDLREV 328
```

```

; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10/782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 674
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-782-096-21

Query Match      22.7%; Score 831; DB 4; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY 4 MSPQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCQG--ISWDEIWE 55
DB 1 MNQYQNKNEYEILESSNNNNMNPYPFADDPNAVKNKNGYKDWNECEGSNISPSAAA 60

QY 56 SVETITSGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLISIRKEVAD 115
DB 61 ITSXIVSIVLKTAKAVASSLA--DSIKSSLGISKTITENNVSQVSMVQVHQIINRRIOE 118

QY 116 SVLSDAIADFDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDIG---OLVYFVKLSERDF 172
DB 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKSNINVTQVVAEAFKTVREF 170

QY 173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVAVQYKAQFPLSAENVRSSELISPS 232
DB 171 FTKLGIYRTSSQITLLPTFTQAANLHLSMLRDVAVMQEGW-----NLQSHI----- 218

QY 233 GCDFTGDIYERLCKTAETNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLD 292
DB 219 -----NYSKELDDALEDTNYCVVYTKGLNALR--GSTAID-WLEFNSFRDMLVLD 270

QY 293 IIAFPYDFEYKPLPHTVELTREIYTDVAVGYSGTYSWLRNPWT-----FNGLEANG 346
DB 271 LVAIFPNYVRYPLSTKISLRKIYDTPVGRDTPS---FGDWTNIGRTLAFNFDLREVE 328

QY 347 TRGGLVTLWSKIGIYNEYVSRV-----FAGVGTGRHYEDYT-KNGIFQRMSTGTT- 396
DB 329 TDSPLVKWLGDMTITVGTADSRYPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTA 388

QY 397 -----SNDLRNIDFQNAVYK--ITSLAIMNLVG--ETTARPEYRVSKADFRVGGPDJNY 448
DB 389 YEDPSTFISNLYD--DIYKLDLRAAAVSTIQAMDIT---FGVSSSRFFDIRGNOLY 442

QY 449 DAGNGLSRMTTESTFPLVLHNSG--VRGPSHRL-----SNAACVYGNRSRVNYGWT 500
DB 443 QS-NKPYPSLPITITFPGESSEGNANDYSHLLCDVKILOEDSSNICGRSLLSHAWTH 501

QY 501 TSLKRENIIEANOITQIPAVKSYIQLNYLANAYTVYIKGT-HTGGDLIRFLRTKSEYNV 559
DB 502 ASLRNNTILPEITQIPAVTAYELR-----GNSSVWAGPGSTGGDLV---KMSYHSV 551

QY 560 YAGGIRLIINNKTAGQSVIRFRYAADKAFF-----SVLYPGGWSNRFVLSLEKSY 613
DB 552 WS---FKYVCSEL---KNYRVRIRYASHGNCQFLMKRVPSTGVAPROWARH---NVQGT 602

QY 614 SGNYDDLYKDFKFAEITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSTTTLE 673
DB 603 S---NSMYEAKYIDIFITTEENNFAFTIDLESG-----DLFIDKIEFIPVSGSAFE 654

QY 674 YEGERDLEKTKNAVNDLFTN 693
|||||:|||||:|||||:

```

```

DB 655 YEGKQNIETKQKAVNDLFIN 674

RESULT 10
US-10-782-570-17
; Sequence 17, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 674
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-782-570-17

Query Match      22.7%; Score 831; DB 4; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY 4 MSPQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCQG--ISWDEIWE 55
DB 1 MNQYQNKNEYEILESSNNNNMNPYPFADDPNAVKNKNGYKDWNECEGSNISPSAAA 60

QY 56 SVETITSGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLISIRKEVAD 115
DB 61 ITSXIVSIVLKTAKAVASSLA--DSIKSSLGISKTITENNVSQVSMVQVHQIINRRIOE 118

QY 116 SVLSDAIADFDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDIG---OLVYFVKLSERDF 172
DB 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKSNINVTQVVAEAFKTVREF 170

QY 173 NEILGSSLRNNAQVLLPTFAQANVQLLLRDVAVQYKAQFPLSAENVRSSELISPS 232
DB 171 FTKLGIYRTSSQITLLPTFTQAANLHLSMLRDVAVMQEGW-----NLQSHI----- 218

QY 233 GCDFTGDIYERLCKTAETNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLD 292
DB 219 -----NYSKELDDALEDTNYCVVYTKGLNALR--GSTAID-WLEFNSFRDMLVLD 270

QY 293 IIAFPYDFEYKPLPHTVELTREIYTDVAVGYSGTYSWLRNPWT-----FNGLEANG 346
DB 271 LVAIFPNYVRYPLSTKISLRKIYDTPVGRDTPS---FGDWTNIGRTLAFNFDLREVE 328

QY 347 TRGGLVTLWSKIGIYNEYVSRV-----FAGVGTGRHYEDYT-KNGIFQRMSTGTT- 396
DB 329 TDSPLVKWLGDMTITVGTADSRYPTSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTA 388

QY 397 -----SNDLRNIDFQNAVYK--ITSLAIMNLVG--ETTARPEYRVSKADFRVGGPDJNY 448
DB 389 YEDPSTFISNLYD--DIYKLDLRAAAVSTIQAMDIT---FGVSSSRFFDIRGNOLY 442

QY 449 DAGNGLSRMTTESTFPLVLHNSG--VRGPSHRL-----SNAACVYGNRSRVNYGWT 500
DB 443 QS-NKPYPSLPITITFPGESSEGNANDYSHLLCDVKILOEDSSNICGRSLLSHAWTH 501

QY 501 TSLKRENIIEANOITQIPAVKSYIQLNYLANAYTVYIKGT-HTGGDLIRFLRTKSEYNV 559
DB 502 ASLRNNTILPEITQIPAVTAYELR-----GNSSVWAGPGSTGGDLV---KMSYHSV 551

QY 560 YAGGIRLIINNKTAGQSVIRFRYAADKAFF-----SVLYPGGWSNRFVLSLEKSY 613

```

```
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-5

Query Match      42.7%; Score 1561.5; DB 4; Length 669;
Best Local Similarity 47.1%; Pred. No. 2.3e-116;
Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;

QY 4 MSPYQKNVEYEILESSNNNTNTPNRYPPANNRDMSTWMDCOGIGWDEIWESEVETITS 63
Db 1 MNSYQNTNEYEILDGSPNNTMSNRYPPAFKDPNIPFNLDACQGRPWQDTSVSDIVTI 60

QY 64 GINLIERPIEPSGGINTLLSIIGKLPNTQTVSALSCDLSIIRKEVADSVLSDATA 123
Db 61 GTYLQFLPEFGGIPGIVPISINKLIPSGQVAALSICDLVSIIRKEVDESVDGVA 120

QY 124 DFDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDIGOLVYVFKLSERDFNEILGGLSRN 183
Db 121 DFGEMTAYODYLHYLEDWLD-----KSNPKLADVVKQFOAREDEFTKLGLAGLSRQ 175

QY 184 NAQVLLPTPAQAANVOLLRLRDVQYKAQWFFLSAENVRSLSLSPNSGCDFTGDYDER 243
Db 176 KABILLPTVQAANVHLLRLRDVAVYKKEW-----GLVCPPLYPGSG---RTDCNER 225

QY 244 LKCKTAETNYCLWYQVGLNOIKQGTGADTWSKKNKFRREMTLAVLDIIAIFPYDPE 303
Db 226 LKAKIKETNYCVGWYKGLDQIQAGTSAEYVSKNFRREMTLAVLDIIAIFPYDPE 285

QY 304 KYPLTHVELTRIYTDVAGYSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKGIYN 363
Db 286 KYPLATSVELTRIYTDVGYSGTYGWERFF--SFNSVEANGTRGPGLVTLWQADIIYS 343

QY 364 EYVS---RYPAGWVGRHYEDYTKNGIIFORMSGTTSNDLRNIDFQNAVYKITSL---A 417
Db 344 HSINLQGLSGWGGTRHYEDFTKNGAGFORMSGTTSNNPRNIFGNTDIFKIISLARYA 403

QY 418 INNLVGETTARPEYRVSKADPRVCGPDLNDYDAGNGLSRMTIESTFPLVLSNGVR--- 474
Db 404 MQPFVGYSI--PRLVSRAEFFTTTLNTFLYEVNSGYSQ-TIESVLP-----GINKDL 454

QY 475 -----GFSHRLSNAACVYVGNRVYVWTHTSLKRENIIEANQITQIPAVKSYLQNYL 529
Db 455 PSRTNYSHRLSNAACVQNETSRVNVFGWTHSMKDNRIYDPKTIQIPAVKAFALPACT 514

QY 530 ANAYTVIKGT-HTGDLIRFLRTKSEYNNAVAGGIRLIINNKTAGQSYRIRFRYAADK 588
Db 515 GVAGGYVTAGPGYTGDDVTL-----PYQA-----SLKIRLTSAPTNKNVRLRYASGG 564

QY 589 AAFPSVLYPGGWSNRVFSLEKSYSGNYDDLKYSDFKFAEITPPLPSNTQMDVEMQA 648
Db 565 PGFPRVERSPSSVSN--ANFSRPATGG-----YSSFDYVDTLVTTFNQSGVEIIQN-- 615

QY 649 NSPQSDNVNVLDKIEFLP-----SNTTILEYEGE-----RDLEKTKNAVNDLFTN 693
Db 616 ---LSGHLIVDKVEFIPIDIQIEKTKCFQEGDICRCBGVQSLTKKIVNSLFIN 669
```

RESULT 8

```
US-10-782-141-20
; Sequence 20, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
```

```
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-20
```

```
Query Match      22.7%; Score 831; DB 4; Length 674;
Best Local Similarity 31.9%; Pred. No. 1.2e-57;
Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;

QY 4 MSPYQKNVEYEILESSNNNTNTPNRYPPANN-----RDMSTWSW-NDCQG--TSWDEIWE 55
Db 1 MNQYQKNVEYEILESSQNMMNPNRYPPADDPNAVMMKNGYKDWVNECEGNSPSPAAA 60

QY 56 SVETITSGINLIEFVIEPSLGGINTLLSIIGKLPNTQTVSALSCDLSIIRKEVAD 115
Db 61 ITSIVSIVLKTAKAVASSLA--DSIKSSLSGSKTITENNVSQVSMVQVHQIINRIQE 118

QY 116 SVLSDAIADFDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDIG---QLVYVFKLSERDF 172
Db 119 TILDGESSLGLVAINRDYLGALAW-----NNKSNINYQTNVAEAKTVEREF 170

QY 173 NEILGGSLSRNAQVLLPTPAQAANVOLLRLRDVQYKAQWFFLSAENVRSLSLSPNS 232
Db 171 FTKLGIYRTSSQITLLPTFTQAANLHLSMLRDVAVYQEGM-----NLQSHI----- 218

QY 233 GCDFTGDIYERLKCKTAETNYCLWYQVGLNQIKQGTGADTWSKFNKFRREMTLAVLD 292
Db 219 -----NYSKELDDALEDYTCVEYTKGLNALR--GSTAID--WLEFNSFRDRMTLMLVD 270

QY 293 IIAIPTVDYFEXYPLTHVELTRIYTDVAGYSGTYSWLRNWPNT-----FNGLEANG 346
Db 271 LVAIPTNPNRYPLSTKLSRKIYTDVPGRTDPS--FGDWTNTRTLANPNDLREVR 328

QY 347 TRGPGLVTLWSKIGIYNEVYSY-----PAGWVGRHYEDYT-KNGIIFORMSGTT- 396
Db 329 TDSPLVKWLGDMTIVTGAIDSYRPTSPGDRIGVWYGNINAFVHTGRTDVMFRQTGDTA 388

QY 397 -----SNDLRNIDFQNAVYK--ITSIAIMNLVG--ETTAPPEYRVSKADPRVCGPDLNY 448
Db 389 YEDPSTFISNILD--DIYKDLRAAAVSTIQAMDIT-----FGVSSSRFFDINGRNQLY 442

QY 449 DAGNGLSRMTIESTFPLVLSNG--VRGSPSHRL-----SNAACVYVGNRVYVWTH 500
Db 443 QS-NKPYPSLPITITFGEESSEGNANDYSHLLCDVKILOEDSSNICGRSLLSHAWTH 501

QY 501 TSLKRENIIEANQITQIPAVKSYLQNYLANAYTVIKGT-HTGDLIRFLRTKSEYNVAV 559
Db 502 ASLDRNNTILPDEITQIPAVTAYELR-----GNSSVWAGPGSGTGDLV-----KMSYHSV 551

QY 560 YAGGIRLIINNKTAGQSYRIRFRYAADKAAFP-----SVLYPGGWSGNRPFVLSKSY 613
Db 552 WS---FKYVCSL---KNYVRIRYASHGNCQFLMKRWPFSTGVAPROWARH---NVQGTG 602

QY 614 SGNVDDLKYSDFKFAEITPPLPSNIIQMDVEMQANSFQSDNVNVLDKIEFLPSNTTILE 673
Db 603 S---NSMYEAPKYLDITITPEENNFAFTIDLESQG-----DLFIDKIEFIPVSGSAFE 654

QY 674 YEGERDLEKTKNAVNDLFTN 693
Db 655 YEGKQNIETKQKAVNDLFIN 674
```

RESULT 9

```
US-10-782-096-21
; Sequence 21, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
```


Db	3	YENKQEYILESSNNTWPNRYFPANDRDNSTWSPNDQCIGISWDEIWSAETITSGID	62
Qy	67	LIEFVIEPSLGGINTLLSIIIGKLIPTNRQTVSALISICOLLSIIRKEVADSVLSDAIADP-	125
Db	63	LIEFLMEPSLGGINTLFSIIIGKLIPTHQSVSALISICOLLSIIRKEVADSVLSDAICRL	122
Qy	126	DGKLKNYREYLSYLGAWLKDGKPLQKTNNSDIGQLVYYPFKLSERDFNEILGSSLSRNN	185
Db	123	DGKLKNYREYLPYLEAWLKDGKPLQKTNNSDIGQLVKYFELSERDFNEILGSSLARNA	182
Qy	186	QVLLLPPTAAQANVOLLILLRDAVOYKQAWPPFLSAENVRSSELSPNSGCDFTGDYYERLK	245
Db	183	QILLPYFCASCCKOLLRLDAVOYEQWPPFLSAENVRSSELSPNSGCDFTGDYYERLK	242
Qy	246	CKTAETVNYCLWYQVGLNQIKQGTGADTWKSNKFRREMTLAVLDIIAIPPTDYDFEKY	305
Db	243	CKIAETDYCEWYQAGLNQIKQAGTGADTWAKFNKFRREMTLVLDIIAIPPTDYDFEKY	302
Qy	306	PLPTHVELTREIYTDVAGYSSTGYSWLRNWPNTFNGLEANGTRGPGGLTWLSKIGIYNY	365
Db	303	PLPTHVELTREIYTDVPVYSSGTYSWLKYWTGAFTLEANGTRGPGGLTWLSRIGIYNEY	362
Qy	366	VSRYPAGWGTREHYEDYTKNGIIFQMSGTTSDNLRNIDFQNAVYKITSILAINLVGFT	425
Db	363	VSRYPGWWGTREHYEDYTTGNGNTFORMSGTTSDNLRDISPNSDIFKIESKAIMNLVGEI	422
Qy	426	TARPEYRYSKADFRVCGPDLNADYAGNGLSRMTIESTFPLVLHSGNVRGP-----SH	478
Db	423	NARPEYRVSRAEFSEFSESTAFIYLDAGNSGLSSMTITSKLP-----GIKNPSPSYDISH	476
Qy	479	RLSNAACVYVYGNRNVVYGWTHTSLKRENIIEANQITQIPAVKYSYLYONLYANAYTVYIK	538
Db	477	RLSNAACVAGAGNSRINVYGWTHTSMSKYNLIYDPKIQIPAVKAFDISD---TGPGQVIA	533
Qy	539	GT-HTGCGDLIRPLRTKSEYNVAYAGGIRLIINNKTAGQSYRTRFYAADKAAPFSVYILY	597
Db	534	GPGTGGGNVSL-----PYYSRLKIRLI--PASTNKNYLVRVRYTSTS---NGRLL	579
Qy	598	PGCGSNRNFVLSLEKY-----SGNVDDLKYSDFKFABIITPPLSPSSINQWDEMQANSQP	652
Db	580	VERNESP-----SIINSYFPLPSTGTGCDSPGYD-----TLVTFNPGVEIILIQNLD	627
Qy	653	SDNVVVLKIEFLPSNTTTLTYEGERDELEKTKNAVNDLF	691
Db	628	TPIN--DKVEIPVNSTALEYEGKSLKKAQDVNDLF	664

```

Qy      646 MQANSFQSDVNVLDKIEFLP-----SNTTLEYEGE-----RDLEKTKNAVNDLFPTN   693
          | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      618 N-----LSGYHLIVDKVEFPIDIQIEKTCQFEGDICRCGVSQSLTEKKKEIVNSLFIN   672

RESULT 7
US-10-782-141-5
; Sequence 5, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782.141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5

```



```

Db      301 DFEKPLPHVLTREIYTDVAGYSSGYSLRWNPNTFNGLEANGTRGPGVLTWLSKIG 360
Qy      361 IYNEVSRFAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLAIMN 420
Db      361 IYNEVSRFAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLAIMN 420
Qy      421 LVGETTARPEYRVSKADPRRVGGPDLDYDAGNNGLSRMTIESTPPLVLSHNGVRGSPSHRL 480
Db      421 LVGETTARPEYRVSKADPRRVGGPDLDYDAGNNGLSRMTIESTPPLVLSHNGVRGSPSHRL 480
Qy      481 SNAACVVGNSRVNRYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGT 540
Db      481 SNAACVVGNSRVNRYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGT 540
Qy      541 HTGGDLIRPLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRPRYAADKAAPFSVLYPGG 600
Db      541 HTGGDLIRPLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRPRYAADKAAPFSVLYPGG 600
Qy      601 WGSNRFVLSKSYSGNYDDLYKSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLD 660
Db      601 WGSNRFVLSKSYSGNYDDLYKSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLD 660
Qy      661 KIEFLPSNTTLEYGGERDLEKTKNAVNDLFTN 693
Db      661 KIEFLPSNTTLEYGGERDLEKTKNAVNDLFTN 693

```

RESULT 2

```

US-10-781-979-5
; Sequence 5, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; PRIOR FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-5

```

```

Query Match      99.6%; Score 3640; DB 5; Length 690;
Best Local Similarity 100.0%; Pred. No. 2.3e-283;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 MSPYQNKNEYEILESSNNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWESVETIISI 63
Db      1 MSPYQNKNEYEILESSNNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWESVETIISI 60
Qy      64 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIIRKEVADSVLSDAIA 123
Db      61 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIIRKEVADSVLSDAIA 120
Qy      124 DFDGKLKNRYEYLYSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRN 183
Db      121 DFDGKLKNRYEYLYSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRN 180
Qy      184 NAOVLLPTFAQANVQLLLRDVQYKAQWPFPLSAENVRSSELISPNSGCDFTGDYDER 243
Db      181 NAOVLLPTFAQANVQLLLRDVQYKAQWPFPLSAENVRSSELISPNSGCDFTGDYDER 240

```

```

Qy      244 LKCKTAETNYCLWYQVGLNQIKOGGTGADTWSKFNKFRREMTLAVLDIIAIPPTDPE 303
Db      241 LKCKTAETNYCLWYQVGLNQIKOGGTGADTWSKFNKFRREMTLAVLDIIAIPPTDPE 300
Qy      304 KYPLPTHVELTREIYTDVAGYSSGYSLRWNPNTFNGLEANGTRGPGVLTWLSKIGIYN 363
Db      301 KYPLPTHVELTREIYTDVAGYSSGYSLRWNPNTFNGLEANGTRGPGVLTWLSKIGIYN 360
Qy      364 EYVSRYFAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLAIMN 423
Db      361 EYVSRYFAGVGTGTHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNDADVYKITSLAIMN 420
Qy      424 ETTARPEYRVSKADPRRVGGPDLDYDAGNNGLSRMTIESTPPLVLSHNGVRGSPSHRLSNA 483
Db      421 ETTARPEYRVSKADPRRVGGPDLDYDAGNNGLSRMTIESTPPLVLSHNGVRGSPSHRLSNA 480
Qy      484 ACVYVGSNRVNYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGTHTG 543
Db      481 ACVYVGSNRVNYGWTHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVVIKGTHTG 540
Qy      544 GDLIRPLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRPRYAADKAAPFSVLYPGGWS 603
Db      541 GDLIRPLRTKSEYNVAVAGGIRLIINNKTAGQSYRIRPRYAADKAAPFSVLYPGGWS 600
Qy      604 NRVFVLSKSYSGNYDDLYKSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLDKIE 663
Db      601 NRVFVLSKSYSGNYDDLYKSDFKFAEIIITPPLPSSNIQMDVEMOANSFQSDVNVVLDKIE 660
Qy      664 FLPSNTTLEYGGERDLEKTKNAVNDLFTN 693
Db      661 FLPSNTTLEYGGERDLEKTKNAVNDLFTN 690

```

RESULT 3

```

US-10-782-141-23
; Sequence 23, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-23

```

```

Query Match      63.7%; Score 2329.5; DB 4; Length 666;
Best Local Similarity 67.2%; Pred. No. 4.5e-178;
Matches 470; Conservative 62; Mismatches 116; Indels 51; Gaps 12;

```

```

Qy      7 YONKNEVEILESSNNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWESVETIISIGIN 66
Db      3 YENKNEVEILESSNNNTNPNRYPPANNRDMSTMSWDCQGISWDEIWESVETIISIGID 62
Qy      67 LIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIIRKEVADSVLSDAIADP- 125
Db      63 LIEFMEPSLGGINTLLSIIGKLIPTNHQSVSALSICDLSIIIRKEVADSVLSDAICRFL 122
Qy      126 DGKLNRYEYLYSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRNA 185
Db      123 DGKLNRYEYLYSYLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEILGGSLSRNA 182

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 11:15:22 ; Search time 168 Seconds
(without alignments)
1723.546 Million cell updates/sec

Title: US-10-781-979-3
Perfect score: 3655
Sequence: 1 MKKMSPYQNKNEYELLESSS.....YEGERDLEKTKNAVNDLFTN 693

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cn2_6/prodata1/pubpaa/us07_PUBCOMB.pap.*
- 2: /cn2_6/prodata1/pubpaa/us08_PUBCOMB.pap.*
- 3: /cn2_6/prodata1/pubpaa/us09_PUBCOMB.pap.*
- 4: /cn2_6/prodata1/pubpaa/us10A_PUBCOMB.pap.*
- 5: /cn2_6/prodata1/pubpaa/us10B_PUBCOMB.pap.*
- 6: /cn2_6/prodata1/pubpaa/us11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3655	100.0	693	5	US-10-781-979-3
2	3640	99.6	690	5	US-10-781-979-5
3	2329.5	63.7	666	4	US-10-782-141-23
4	2329.5	63.7	666	4	US-10-782-096-23
5	2329.5	63.7	666	5	US-10-781-979-25
6	1571.5	43.0	672	4	US-10-782-141-3
7	1561.5	42.7	669	4	US-10-782-141-5
8	831	22.7	674	4	US-10-782-141-20
9	831	22.7	674	4	US-10-782-096-21
10	831	22.7	674	4	US-10-782-570-17
11	831	22.7	674	5	US-10-783-417-15
12	831	22.7	674	5	US-10-781-979-22
13	747	20.4	1151	6	US-11-018-615-13
14	747	20.4	1156	4	US-10-099-285-70
15	747	20.4	1156	6	US-11-018-615-12
16	725	19.8	1167	4	US-10-089-678-1
17	724	19.8	659	5	US-10-782-141-22
18	724	19.8	659	5	US-10-781-979-24
19	713.5	19.5	1206	4	US-10-032-717-2
20	713.5	19.5	1206	4	US-10-414-637-2
21	713.5	19.5	1206	4	US-10-606-320-2
22	713.5	19.5	1206	4	US-10-746-914-2
23	712	19.5	802	4	US-10-428-961-30
24	707.5	19.4	719	5	US-10-926-819-30
25	707.5	19.4	719	5	US-10-926-819-31
26	705.5	19.3	1228	5	US-10-926-819-8
27	702.5	19.2	1228	4	US-10-809-953-10

28	700	19.2	710	4	US-10-428-961-42	Sequence 42, Appl
29	690.5	18.9	675	4	US-10-782-141-21	Sequence 21, Appl
30	690.5	18.9	675	4	US-10-782-096-22	Sequence 22, Appl
31	690.5	18.9	675	5	US-10-781-979-23	Sequence 23, Appl
32	686	18.8	1227	4	US-10-428-961-63	Sequence 63, Appl
33	683	18.7	682	4	US-10-782-096-2	Sequence 2, Appl
34	683	18.7	1207	3	US-09-988-462-7	Sequence 7, Appl
35	681	18.6	1186	3	US-09-826-660-23	Sequence 23, Appl
36	679	18.6	719	4	US-10-782-020-10	Sequence 10, Appl
37	679	18.6	719	4	US-10-782-141-8	Sequence 8, Appl
38	679	18.6	719	4	US-10-782-096-10	Sequence 10, Appl
39	679	18.6	719	4	US-10-782-570-7	Sequence 7, Appl
40	679	18.6	719	5	US-10-783-417-5	Sequence 5, Appl
41	679	18.6	719	5	US-10-781-979-10	Sequence 10, Appl
42	679	18.6	719	5	US-10-478-243A-28	Sequence 28, Appl
43	679	18.6	719	5	US-10-478-243A-31	Sequence 31, Appl
44	679	18.6	719	5	US-10-926-819-11	Sequence 11, Appl
45	679	18.6	719	5	US-10-926-819-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-781-979-3
; Sequence 3, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-781-979-3

Query Match	100.0%;	Score 3655;	DB 5;	Length 693;
Best Local Similarity	100.0%;	Pred. No. 1.5e-284;	Mismatches 0;	Indels 0;
Matches 693;	Conservative 0;			Gaps 0;
Qy	1	MKKMSPYQNKNEYELLESSSNTNTPNRYPPANNRDMSTMWDCQGISWDIWSVETI	60	
Db	1	MKKMSPYQNKNEYELLESSSNTNTPNRYPPANNRDMSTMWDCQGISWDIWSVETI	60	
Qy	61	TSIGINLIEFVIEPSLGGINTLLSIGLIPNROTVSALSICDLLSIIRKEVADSVLSD	120	
Db	61	TSIGINLIEFVIEPSLGGINTLLSIGLIPNROTVSALSICDLLSIIRKEVADSVLSD	120	
Qy	121	AIADPDGKLKNRYEYLSYLGAWLKDGPLOKTNNSDYGQVYKQWPFELSAENVRSLEISPNSGCDPTGDY	180	
Db	121	AIADPDGKLKNRYEYLSYLGAWLKDGPLOKTNNSDYGQVYKQWPFELSAENVRSLEISPNSGCDPTGDY	180	
Qy	181	SRNNAQVLLLPPTFAAANVQLLLRDVQYKQWPFELSAENVRSLEISPNSGCDPTGDY	240	
Db	181	SRNNAQVLLLPPTFAAANVQLLLRDVQYKQWPFELSAENVRSLEISPNSGCDPTGDY	240	
Qy	241	YERLKCKTAETNYCLYQVGLNQIKQGGTADTWSKFNKFRREMTLAVLDIIAIFPTY	300	
Db	241	YERLKCKTAETNYCLYQVGLNQIKQGGTADTWSKFNKFRREMTLAVLDIIAIFPTY	300	
Qy	301	DFEKPLPETHVELTREIYTDVAGYSSGYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIG	360	

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Db 223 -----YPQNDIDL---FYKEQVSVTARYSDHCVQVYNAGLNKLR--GTGAKQWV 266
QY 278 KFNKFRREMTLAVLDDIATPPTDFEYKPLPHTVELTREIYTDVAG-YSSGTYSWLRNWP 336
Db 267 DYNRFRREMNVMVLDLVALFPNDYDARIYPLETNAELTREIFDPVGSYVTQGSSTLISWY 326
QY 337 N-----TFNGLEANTRGPGGLVWLKIGIYNEY-----VSRYFAGWVGRHYEDYTKG 385
Db 327 DMIPAAALPSESTLE-NLLRPDPFTLLQEIWMYTSFRQNGTIEYYNWGGQRLTLSYIYG 385
QY 386 NGIFQRMGTTSNDLRNIDFQNDADVYKI-----TSLAIMNLVGETTAR 428
Db 386 SS-FNKYSGVLAGAEDIIPVGQNDIYRVVWYIIGRYTNSLLGVNPTVFYFSNNTQKTYSK 444
QY 429 PEY---RVSKADFRVCGPDL---NYDAGNGLSRMT---IESTFPLVLHSGVGRGFSHR 479
Db 445 PKQFAGGIKTID-----SGEELTYENYQSYGHRVSYITSFEIKSTGGTVL---GV----- 491
QY 480 LSNAACVVYGNRSRVNVYGWTHTSIKRENIIEANQITQIPAVKSYYLQNYLANAYTYVIKG 539
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVWNFQEG 535
QY 540 THTGGDLIRFLRTKSEYNAYAGG-----IRLIINNKTAGQSYRIRFRYAADKAAFFSV 594
Db 536 LYNGGPVMKL-----SGSGSQVINLRVATDAKGASQRYRIRIRYASDRACKFTI 584
QY 595 YLYPGGWSNRFSVLSKSYSGNY-----DDLKYSDFKFAEITTPPLPSSNIQMDVE 645
Db 585 -----SSRSPENPATYSASIAYTNTMTSNASLTYSTPAYAE-----SGPINLGIS 629
QY 646 MQANSFQSDV-----NVVLDKIEFLPSNTTILEYEGEDLEKTKNAVNDLFTN 693
Db 630 GSSRTFDISITKEAGAAANLYIDRIEFIPVNTL---FEABEDLDVAKKAVNGLFTN 681

Search completed: December 15, 2005, 11:15:12

Job time : 193 secs

XX WPI: 1993-076511/09.
 DR N-PSDB; AAQ36866.
 XX
 PT New strain of *Bacillus thuringiensis* serovar japonensis - producing toxin
 PT active against coleoptera larvae.
 XX
 PS Claim 5; Page 28; 48pp; English.
 XX
 CC The protein sequence is that of a toxin active against Coleoptera that is
 CC produced from a pure culture of *Bacillus thuringiensis* serovar japonensis
 CC variety Buibui (FERM BP-3465). The toxin is a delta-endotoxin which has a
 CC mol. wt. of ca. 130 kD. It is useful for control of coleoptera larvae
 CC e.g. it is effective against *Anomala cuprea* but has little effect on
 CC Lepidoptera. The toxin can be used as B.t. spores or crystals, as opt.
 CC treated cells (B.t. or transformed microorganisms) or it is expressed by
 CC plants. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 1149 AA;

Query Match 19.9%; Score 728.5; DB 2; Length 1149;
 Best Local Similarity 29.9%; Pred. No. 1.3e-48;
 Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;
 QY 4 MSPYONKNEYEILESSNNTNTPN--RYPFANNRDMSTMWDCOGISWDE----- 52
 DB 1 MSP-NNQNEYEILDALSPVSDNSIRYPLANDQNTLQNMNYKDYLNKTESTNAELSRN 59
 QY 53 --IWESVETITSGINLIEFVIE----PSLGGINTLL-SIIGKLIPTNRQTVSALSICDL 105
 DB 60 PCTFISAQDAVGTGIDIVSTIISGLGIPVLGEVFSILGSLGLWPSNNENVMQIFMNRV 119
 QY 106 LSIIRKEVADSVLSDAIADFDGKLKNYR---EYLSYLGAWLKQKPKLQKTNNSDIGQLV 162
 DB 120 BELIDQKILDSVRSRAIAD----LANSRIAIVEYQNALEDWRKNP---HSTRSAAL---- 168
 QY 163 YVFKLSERDFN--ETLG---GSLSRNNAQVLLPFAQAAVQLLLRDAVQYKQWPPF 217
 DB 169 -----VKERFGNAELRTNMGSFQNTYETPLPTFYAQASLUHLVMDVQIYKQW-- 222
 QY 218 LSAENVRSSELISPNSGCDFTGDIYERLCKTAETNYCLYWTQVGLNQIKQGGTGADTWS 277
 DB 223 -----YFQNDIDL--FYKEQVSYTARYSDHCQVQWYNAGLNKLR--GTGAKQWV 266
 QY 278 KENKREMTLAVLDIIAIPPTDEKYPPLPHVELTRIIYTDVG--YSSGYYSWLNRWP 336
 DB 267 DYNFRREMNMVLDLVALFPNDARYPLETNAELTREIFTDPVGSYVTGQSSTLISWY 326
 QY 337 N-----TFNGLEANGTRGPGVLTWLSKIGIYNEY---VSRYPAGWVGRHYEDYTKG 385
 DB 327 DMIPALPFSFLE-NLLRKPDPFFLLQBEIRMTSFRQNGTIEYNYWGGQLTSLIYVG 385
 QY 386 NGIFORMSGTTSNLRNIDFQNAVYKI-----TSLAIMNLVGETTAR 428
 DB 386 SS-FNKYSGLAGAEIIPVGQNDIYRVVVTYIGRVYTNLSLLGVNVPVTFYSNNTQKTSK 444
 QY 429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---ISTPLVLHSGVGRPSHR 479
 DB 445 PKPQAGGIKTID----SGEELTYENQSYSHRVSYITSFEIKSTGTGTVL---GV----- 491
 QY 480 LSNAAVYVGNRVNRYGWTHTSLKRENIIEANQTOIPAKVSYVLYQLNAYTVYVIGK 539
 DB 492 -----VPFQTHSASRNFIYATKISQIPINKA---SRTSGGAVNWFQEG 535
 QY 540 THTGDLIRFLRTKSEYNAVYAGG-----IRLIINNTAGOSYRIRFRYAADKAAFFSV 594
 DB 536 LYNQGPVVKL-----SSGSGQVINLRVATDAKQASQYRIRIRYASDRAGKFTI 584
 QY 595 YLPGWGNRFRVLSLEKSYSGNY-----DDLKYSDFKFAEITPPLPSNTOQMDVE 645
 DB 585 -----SSRSPENPATYSASIAVTNTMTSNASTYSTYFAVAE-----SGPINLGIS 629

QY 646 MQANSFQSDV-----NVVLDKLEPLSPNTTLEYEGERDLEKTKNAVNDLFTN 693
 DB 630 GSSRTFDISITKEAGANLYIDRIEPIPVNTL---FEABEDLDVAKVANGVLFNTN 681
 RESULT 15
 AARS1692
 ID AARS1692 standard; protein; 1149 AA.
 XX
 AC AARS1692;
 XX
 DT 16-OCT-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX
 DE B.thuringiensis serovar Japonensis insecticidal protein.
 XX insecticidal protein; Coleoptera larvae; Buibui fungus.
 XX
 OS *Bacillus thuringiensis*; (serovar Japonensis).
 OS strain Buibui).
 XX
 FH Key Location/Qualifiers
 FT Region 751..766
 FT /note= "amino acids 751-766 are not given in the
 FT specification and so have been decoded from AAQ58975"
 XX
 JP06065292-A.
 PN 08-MAR-1994.
 PD
 XX 11-AUG-1992; 92JP-00213886.
 XX
 PR 11-AUG-1992; 92JP-00213886.
 XX
 PA (KUBI) KUBOTA CORP.
 XX
 DR WPI: 1994-121220/15.
 DR N-PSDB; AAQ58975.
 XX
 PT Insecticidal protein and DNA from *Bacillus thuringiensis* serovar
 PT Japonensis strain Buibui - useful in insecticides against Coleoptera
 PT insects.
 XX
 PS Claim 1; Page 9-13; 18pp; Japanese.
 XX
 CC This insecticidal protein has activity against Coleopteran insect larvae
 CC and has been isolated from *Bacillus thuringiensis* serovar japonensis
 CC strain Buibui. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 1149 AA;

Query Match 19.9%; Score 728.5; DB 2; Length 1149;
 Best Local Similarity 29.9%; Pred. No. 1.3e-48;
 Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;
 QY 4 MSPYONKNEYEILESSNNTNTPN--RYPFANNRDMSTMWDCOGISWDE----- 52
 DB 1 MSP-NNQNEYEILDALSPVSDNSIRYPLANDQNTLQNMNYKDYLNKTESTNAELSRN 59
 QY 53 --IWESVETITSGINLIEFVIE----PSLGGINTLL-SIIGKLIPTNRQTVSALSICDL 105
 DB 60 PCTFISAQDAVGTGIDIVSTIISGLGIPVLGEVFSILGSLGLWPSNNENVMQIFMNRV 119
 QY 106 LSIIRKEVADSVLSDAIADFDGKLKNYR---EYLSYLGAWLKQKPKLQKTNNSDIGQLV 162
 DB 120 BELIDQKILDSVRSRAIAD----LANSRIAIVEYQNALEDWRKNP---HSTRSAAL---- 168
 QY 163 YVFKLSERDFN--ETLG---GSLSRNNAQVLLPFAQAAVQLLLRDAVQYKQWPPF 217
 DB 169 -----VKERFGNAELRTNMGSFQNTYETPLPTFYAQASLUHLVMDVQIYKQW-- 222
 QY 218 LSAENVRSSELISPNSGCDFTGDIYERLCKTAETNYCLYWTQVGLNQIKQGGTGADTWS 277

Db 190 IGTIVSLITAPSLTGLISIVYDLIGKVLGGSGQSISDLSDICDLLSIIDLRVSQVLND 249
 Qy 121 ATADFGKLVNREYVSLVGLWLDGKPKLOKTNNSDQVLYVFKLSERDNEIL----- 176
 Db 250 GIADFNGLVLLRN-YLEALDSWKN-----PNSASABELTRFRDIADSEFDRLTRGS 302
 Qy 177 ---GGSLRNNAQVLLPTFAQANVQLLLLRDQVQKAW-----FPFLSAENVRSELI 228
 Db 303 LINGGLARQNAQVLLPFSASAPFHLILLLRDQVQKAW-----FPFLSAENVRSELI 362
 Qy 229 SPNSGCDFTGDYERLCKTAEYVYVYVGLNQIKOGGTGADTWSKFNKFRREMTL 288
 Db 363 E-----LYDYCVHYNKGFNELRQRTSATWLEFHYRREMTL 402
 Qy 289 AVLIIAIPPTDFEYKPLPHTVELTREYTTAVGY-----SSGTSVWLR--NWPNTFNL 342
 Db 403 MWLDIVASFSSLDITNYPIETDFQLSRVITDPIGFVHRSSLRGSEWFSFVNAN--FSDL 461
 Qy 343 EANGTRGPGVLVWLSKIGIYNEVSRYPAG-----WVGTREYEDYTKGNGIFORMSGT 395
 Db 462 E-NAIPNPRPSWFLNMIISTGSLTPVSPSTDRARVWYGSRRDISPANSQIFTELISQ 520
 Qy 396 TSNLNRNIDFQNAVYKITSIAIMNLVGETTARPEYRVSKADPRRVGGPDLNDAGNGL 455
 Db 521 HTTATQTLGRN--IPRVDQA--CNL-NDTT-----YGVNRAVF-----YHDASEGS 563
 Qy 456 SRMTIESTFPLVHNGVRGP-----SHRLSNAACVYVY----- 489
 Db 564 QRSVYEG-----YIRTGIDNPRVQNTYLPGENSDIPTPEYTHILSTINLTGGLRQV 619
 Qy 490 ---NSRVNVYGTWTHSLKRENIIEANQITQIPAVKSYVLYQLANAVTYVIKGTGSD 545
 Db 620 ASNRSSLVWYGTWTHSLKRENIIEANQITQIPAVKSYVLYQLANAVTYVIKGTGSD 545
 Qy 546 LIRPLRTKSEYNAVYAGGIRLIINNKTAQSYRIRFRYAADKAAPFVYLYPGWGSNR 605
 Db 676 LLQ-----RTDHGSL-----GVLRVQPLHLRQYRIRVYASTNIRLSV-----NGS 719
 Qy 606 FVSLKSYSGNY-----DDLKYSDFKAEIITPPLP--SSNTQMDVEHQANSFQSDVNVLDK 661
 Db 720 FTISQNLPSWRLGDELYGSFAIREFTSIRPTASPDQIRLTIEPSFIQEVYV--DR 777
 Qy 662 IEFLPSNTTLEVEGERDELEKTKNAVNDLFT 692
 Db 778 IEFIPVNPTR-----EAKEDLEAAKAVASLFT 805
 RESULT 12
 AAW06417
 ID AAW06417 standard; protein; 1169 AA.
 XX AC AAW06417;
 XX DT 16-OCT-2003 (revised)
 XX DT 28-JAN-1997 (first entry)
 DE Antiscarab pest toxin 50C(b).
 XX KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;
 KW larval stage insect; grain; tuberous crop; white grub; chafer grub;
 KW cyclocephala; popillia.
 XX OS Bacillus thuringiensis; strain kumamotoensis.
 XX PN US5554534-A.
 XX PD 10-SEP-1996.
 XX PF 30-SEP-1994; 94US-00315468.
 XX PR 16-DEC-1991; 91US-00808316.
 PR 30-JAN-1992; 92US-00828430.
 PR 01-FEB-1993; 93US-00014941.

XX (MYCO) MYCOGEN CORP.
 PA Focerrada L, Narva KE, Michaels TE;
 PI WPI; 1996-424659/42.
 DR N-PSDB; AAT43221.
 XX New nucleic acid encoding B.thuringiensis toxin active against scarab(s)
 PT - also related toxin and transformed microbes, effective against adult
 PT pests and their larvae.
 XX Claim 2; Col 29-36; 24pp; English.
 XX AAW06417-W06419 represent toxins that are active against scarab pests.
 CC The DNA encoding this sequence was isolated from the Bacillus
 CC thuringiensis strain kumamotoensis. Insects in the family Scarabaeidae
 CC constitute a serious pest control problem, especially when destructive
 CC larval stage insects infest high value turf found in golf courses,
 CC playing fields and lawns. The larvae of many species also attack grains,
 CC tuberous crops, and ornamentals. The larvae are known as white grubs, or
 CC chafer grubs, and can be found in decaying organic matter, or in the soil
 CC where they consume plant roots. In Europe and the U.S. populations of
 CC these larvae and adults have developed resistance to chemical
 CC insecticides such as the organochlorines and DDT. These toxin sequences,
 CC and intact cells that are capable of expressing these proteins, can be
 CC used to control many pests of the family scarabaeidae, such as species of
 CC Cyclocephala, and Popillia. The toxins are active against larvae (present
 CC in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS
 CC field)
 XX SQ Sequence 1169 AA;
 Query Match 20.4%; Score 745; DB 2; Length 1169;
 Best Local Similarity 29.4%; Pred. No. 6.6e-50;
 Matches 217; Conservative 142; Mismatches 274; Indels 104; Gaps 31;
 Qy 4 MSPQNKNEYEILES--SSNNTVTPNRYPPAN--NRDMSTWSWDCQGIS-----W 50
 Db 1 MSP--NNQNEYIIDIATPSTSVNSNRYPPANEPTNALQNDYDKDYLKMSAGNVSEYPGS 59
 Qy 51 DEIVESVETITSIGINLIEFVIE-----PSLGGINTLLS-IIGKLIPTRKQTSALSICDL 105
 Db 60 PEVFLSEQDAKAAIDIVGKLLTGLGVFPVGPVLSLYTQILDILWPSQKSWEIFEMQV 119
 Qy 106 LSIIRKEVADSVLSDAIDFDPKLVNRYEYLYSGLAWLKD---GKPLQKTNNSDIGQLV 162
 Db 120 EELINQKIAEYARNKALSELEGNNY-QLYLTALKEENKPNPGRSALRDVNR----- 172
 Qy 163 YPFKLSERDFNEILGGLSRNNAQVLLPFAQANVQLLLLRDQVQKAWFPFLSAEN 222
 Db 173 ---FEILDSLFTQYM--PSFRVTNFEVPFLTVTMAANLHLLLRDASIFGEEM--GLSTST 227
 Qy 223 VRSELI SPNSGCDFTGDYERLCKTAEYVYVYVGLNQIKOGGTGADTWSKFNK 282
 Db 228 I-----NNYINRQMKLTAEYSDHCWKWYETGLAKLK--GSSAKQWIDYNOF 271
 Qy 283 REMTAVLDIIAIPPTDFEYKPLPHTVELTREYTTAVGYSS--GTYSMLRNWNPNTFN 340
 Db 272 RREMTLTVDVVALPFSNVDTRTYPLATTATQLTREYVTDPLGAVDVPNIGSWYDKAP-SFS 330
 Qy 341 GLEANGTRGPGVLVWLSKIGIYNEVY-----RYFAGWVGTREHYEDYTKGNGIFORMSGT 396
 Db 331 EIEKAAIRPPHFVDYITGLTYTKRSTSDRYMYWAGHQISYKHICTSTFTQMYGTN 390
 Qy 397 SN--DLRNIDFQNAVYKITS--LAIMNLVGETTARPEYRVSKADFRVVG-----GPDLN 447
 Db 391 QNLQSTSNFDTNVDIYKTLNSGAVLLDIVPGYTYTFFGMPETEFPMVNLNTRKTLT 450
 Qy 448 YDAGNGLSRMTIESTFPLVHLSNG-----VRGFSHRLSNAACVYVYVYNSR---YVYVGTWTH 501
 Db 451 YKPASKDIIDTRDSELELPETSQPNVYESVSHRLGHT-FIYSSSTSTYVYVPSWTHR 509

Qy	9	NKNEYELLESSNNNTNPN--RYPPANNRDMSTMWNCQG---ISW-DEIWESVETTTS	62
Db	2	NONKHGIAGNCGCASDDVAKYPIPLANNPYSSALNLSNCSIIILNWINIIGDAAKEAVS	61
Qy	63	IGINLIEFVIPSJGG-INTLLSIIGKLI-PINROTYSALSICDILLSIRKEVADSVLSD	120
Db	62	IGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSGOSISDLSICDILLSIDLRVOSQVLND	121
Qy	121	AIADFDGKLKNRYEYLLSYLGAWLKDGGKPLQKTNNSDICQLVYFVKLSERDFNEIL---	176
Db	122	GIADFGSGLLYRN-YLEALDSWNKN-----PNSASAEELRTRFRIADSEFDRILTRGS	174
Qy	177	---CGSLSRNNAQVLLLPFPQAANVQULLLRDAVOYKAQM-----FPFLSAENVRSBL	228
Db	175	LTNGGSLARQNAQIILLPSPASAAFFHLLLRDLATRYGTNMGWLYNATPFPYQSKLVELI	234
Qy	229	SPNSGCDPTGDIYERLKCKTAETNYCLYVYQVGLNOIKQGTGADTWSKKNKPFREMTL	288
Db	235	E-----LYTDYCVHWNRGFNELRQGTSTAWLEFHRYRREMTL	274
Qy	289	AVLDIIAIFPTYDFEKYPLPHTVELTREIYTDVAGY---SSGTYSWLR--NWPNTFNGL	342
Db	275	MVLOIVASFSSLDITNYPIETDFQLSRVIYTDPIGFVHRSSLRGSSWFSFVNRA--FSDL	333
Qy	343	EANGTRGGLTWLSKIGIYNEYSRYFAG-----WVGRHYEDYTKGNGIPFORMSGT	395
Db	334	E-NAIPNRPSPFWFLNNMIISTGSLTLPVSPSTRARVWYGRDRISPANSQOFITELISQ	392
Qy	396	TSNDLRNIDFONADYVYKITSIAIWNLVGETTARPEYRVSKADFRVGGPDLYDAGNGL	455
Db	393	HTTATQTLGRN--IFRVDSQA-CNL-NDTT-----YGVNRAVF-----YHDASEGS	435
Qy	456	SRMTIESTFPLVLHSHNGVRGP-----SHRLSNAACVVYVG-----	489
Db	436	QRSVYEG---YIRTTGIDNRVQVNIINYLPGENSDIPTPETHYLSTTINLTGLRQV	491
Qy	490	-----NSRVVYGWTHTSUKRNIETANOITQIPAVKSYLQNYLANATYVIKTHGTGSD	545
Db	492	ASNRSSLLVMYGWTHSKSLARNNTINPDRIITPLTK-----VDTRGTGVSYNDPFGIGA	547
Qy	546	LIRFLRNTKSEYNAYVAGGIRLIINNKTAGOSYRIRFPAADKAAFFSVLYLPGCWGNSR	605
Db	548	LLQ-----KTDHGSL-----GVLRVQFPLHLRQOYRIRVYASTTNIRLSV-----NGS	591
Qy	606	FVSLKESYSGNY---DDLKYSDFKFAEIIITPPLP-SSNIQMDVEQAQNSFOSDVNVLDK	661
Db	592	FGITISQNLPSMRLGEDLRVGSFAIRENTSIRPTASPDQILRTIEPFSFIQEYV--DR	649
Qy	662	IEFLPSNTTTLLEYGERDLEKTKNANDLFT	692
Db	650	IEFTVPNPTN-----EAKEDLEAKKAVASLFT	677

RESIST. T. 8

RESULI 8
AAW46856

AAW46856
ID AAW46856 standard; protein; 1156 AA.

0
1
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9

AAW46856:

XX
CY
'0609FMYZ

DT 11-JUN-1998 (first entry)

XX
9667-NOV-77 (TJTB ENLJ)
19 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 XX
DE
Bacillus thuringiensis toxin designation

DE
XX
XX

Toxin: Tetrodotoxin

KW Toxin; Lepid

KW Hellothis viz
vz

XX 01-JUL-1996; 96US-00674002.
XX (MYCO) MYCOGEN CORP.
XX
XX Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
PI
XX
XX WPI; 1998-086971/08.
XX N-PSDB; AAV16515.
XX
XX New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes
PT encoding toxins which are active against lepidopteran pests such as the
PT Black cutworm.
XX
XX Claim 34; Page 82-86; 183pp; English.
XX
XX The present sequence represents a *Bacillus thuringiensis* toxin designated
CC 86BB1(a) which is active against lepidopteran pests. The toxin isolates
CC can be used for the control of lepidopteran pests such as *Agrotis ipsilon*
CC (black cutworm), *Heliothis virescens* and *Helicoverpa zea*. PCR primers and
CC probes can be derived from the polynucleotide encoding the toxin and used
CC for the amplification and detection of other toxin-encoding sequences
XX
XX Sequence 1156 AA; SQ

XX
PF 01-JUL-1997; 97WO-US011658.

PR 20-FEB-2003; 2003US-0448810P.
 PR 20-FEB-2003; 2003US-0448812P.
 PR 19-FEB-2004; 2004US-00781979.
 PR 19-FEB-2004; 2004US-00782020.
 PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 XX
 PA (ATHE-) ATHENIX CORP.
 XX
 PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 XX WPI; 2004-635574/61.
 XX
 DR
 XX
 XX
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX
 XX
 PS Example 6; SEQ ID NO 47; 178pp; English.
 XX
 CC This sequence represents a delta-endotoxin crystal protein. This protein
 CC was included in the scope of the invention as a comparison to the delta-
 CC endotoxins of the invention. Some of the delta-endotoxin coding sequences
 CC of the invention have alternative start codons, producing more than one
 CC protein from a single open reading frame. The nucleic acid sequences of
 CC the invention are useful in DNA constructs or expression cassettes for
 CC transformation and expression in plants and bacteria. The nucleic acids
 CC and corresponding polypeptides are useful for killing lepidopteran or
 CC coleopteran pests. Compositions containing the delta-endotoxins of the
 CC invention, and methods for their production, are useful for the
 CC production of organisms with pesticide resistance, specifically bacteria
 CC and plants. These organisms are useful for generating altered or improved
 CC delta-endotoxin or delta-endotoxin-associated proteins that have
 CC pesticidal activity, or for detecting the presence of delta-endotoxin or
 CC delta-endotoxin-associated proteins or nucleic acids in products or
 CC organisms.
 XX
 SQ Sequence 674 AA;

Query Match 22.7%; Score 831; DB 8; Length 674;
 Best Local Similarity 31.9%; Pred. No. 3.9e-57;
 Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;
 QY 4 MSPYQNKNEYEILESSNNNTNPNRYPPANN-----RDMSTMSW-NDCOG--ISWDELWE 55
 DB 1 MMYQNKNEYEILESSNNMNNPNRYPPADPNAMKNGNYKDWYNECEGNSPSPAAA 60
 QY 56 SVETITSGINLIEFVIEPSLGGINTLSIIIGKIPTNRTQVTSALSI CDLLSIIRKEVAD 115
 DB 61 ITSKIVSIVKTLAKAVASSLA--DSIKSLGSIKTITENNVSQVSMVQVHQIINRTOE 118
 QY 116 SVLSDAIADFDGKLNRYEYLYSILGAMUKOGKPLQKTNNSDIG---QLVYVFKLSERDF 172
 DB 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKSNINYQTNVAEAFKTVREF 170
 QY 173 NEILGSSLRNNAQVLLPTFAQAANVQLLLARDVAOVYKAQWFFLSAENVESELSISNS 232
 DB 171 FTKLGIYRTSSQTLTPTFOAANLHLSMURDAVMYQEGW-----NLQSHI----- 218
 QY 233 GCDFTGDYVERLKCTAETNYCLWYQVGLNQIKQGGTGADTKGFKNFREMTLAVLD 292
 DB 219 -----NYSKELDDALEDTNYCEVYTKGLNALR-GSTAID-WLEFNSFRDWTLMVLD 270
 QY 293 IIAIPTDYDFEKYPLPHTVELTREIYTDAGVYSGTYSWLRNPNVT-----FNGLEANG 346
 DB 271 LVAIFFNPNFVRYPLSTKISLRKIYTDVGRDTSPLS--FGDWTNTGRTLANFNDLREV 328
 QY 347 TRGPGIATVLSKIGLYNEVSVY-----FAGWVGTHYEDYT-KGNIGIFQMSGTT- 396
 DB 329 TDSPLSLVWLGMWTIYTGDAISYRPTSPGDRIGVWYGNINAFYHGTGTDVVMFROGTDA 388
 QY 397 ----SNDLRNIDFQNAVYK--ITSIAIMNLVG--ETTARPEYRVSKADFRVRGPGDLNY 448

DB 389 YEDSTFISNLYD--DIYKLDLRAAAVSTTQGMDDT-----FGVSSSRFFDIRGRNOLY 442
 QY 449 DAGNNGLSRMTIESTFPLVLHNSG-VRGPSHRL-----SNAACVVYGNRNVYGWTH 500
 DB 443 QS-NKPYSLPITITTPGEESEGNANDYSHLLCDVKILQEDSSNICGRSSLLSHAWTH 501
 QY 501 TSLAKRENIIEANQITQIPAVKSYVLYONLANAYTVVINGT-HTGGDLIRFRTKSEYNAY 559
 DB 502 ASLDRNNTILPDEITQIPAVTAYELR-----GNSVWAGPGSTGGDLV-----KMSYHSV 551
 QY 560 YAGGIRLIINNKTAGOSYRIRFRYAADKAAFF-----SVLYPGWGSNRFVSLEKSY 613
 DB 552 WS---FKYVCSEL---KNYRVIRYASHGNCQFLMKRWPGTGVAPQWARH---NVQGTG 602
 QY 614 SGNVDDLKYSFKPAEIIITPPLPSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTLE 673
 DB 603 S---NSMRYEAFKVLIDITITPEENNFAFTIDLESYG-----DLFIDKIEFTIPVSGSAFE 654
 QY 674 YEGERDLEKTKNAVNDLFTN 693
 DB 655 YEGQNIEKTKAVNDLFIN 674
 RESULT 7
 ID AEA81457 standard; protein; 1151 AA.
 XX AEA81457;
 XX 25-AUG-2005 (first entry)
 DE Bacillus thuringiensis Cry9 protein, cryaa2, SEQ ID NO: 13.
 KW Transgenic plant; pesticide; genetically engineered microorganism; cry9;
 KW endotoxin.
 XX Bacillus thuringiensis.
 XX US2005138685-A1.
 XX 23-JUN-2005.
 XX 21-DEC-2004; 2004US-00018615.
 XX 22-DEC-2003; 2003US-0531807P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Flannagan RD, Abad AR;
 XX WPI; 2005-444221/45.
 XX
 PT New isolated nucleic acid encoding a polypeptide having pesticidal
 PT activity, useful for controlling pests, especially plant pests such as
 PT European corn borer, diamond-back moth or fall armyworm.
 XX Disclosure; SEQ ID NO 13; 114pp; English.
 CC The present invention relates to the Bacillus thuringiensis Cry9-family
 CC genes that encode delta-endotoxins having pesticidal activity against
 CC insect pests. The invention is useful for producing pesticidal
 CC compositions for controlling pests in plant such as European corn borer,
 CC diamond-back moth or fall armyworm. The invention is also useful in
 CC production of transgenic plant. The present sequence is the Bacillus
 CC thuringiensis Cry9 protein.
 XX Sequence 1151 AA;

Query Match 20.4%; Score 747; DB 9; Length 1151;
 Best Local Similarity 30.6%; Pred. No. 4.4e-50;
 Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

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RESULT 5
ADR89417
ID ADR89417 standard; protein; 669 AA.
XX
AC ADR89417;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 alternative protein.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX
DR N-PSDB; ADR89416.
XX
DR WPI; 2004-635574/61.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 12; SEQ ID NO 29; 178pp; English.
XX
CC This sequence represents an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 669 AA;
Query Match 42.7%; Score 1561.5; DB 8; Length 669;
Best Local Similarity 47.1%; Pred. No. 1.6e-115;
Matches 338; Conservative 107; Mismatches 197; Indels 75; Gaps 18;
XX
QY 4 MSPYQKNKEVEILESSNNNTNPNRYPFANNRDMSTMWDCQGISWDBIWSVETITS 63
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MNSYQNTNEVEILDGSPNNMNSRYPFAKDPNIPFNILDAQGRPQDTWSVSDIVTI 60

```

```

QY 64 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSDAIA 123
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GTYLIOQLLEPGIGGIPVIFSIINKLIPSSGQVAALSICDLVSIIRKEVDESVLSDGVA 120
QY 124 DFDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIGOLVYFVKLSERDFNEILGGISLRN 183
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 DFEGETAYQDYLYLHYLEDWLT-----KSNPKKJADVVVKQFQAREDFTKLJAGLSURQ 175
QY 184 NAQVLLPTFAQAANVQLLLRDVAQYKAQWEPFLSAENVRSSELISNSGCDFTGDIYER 243
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 KAEILLPTVQAANVHLLLRDVAVKYKKEW-----GLVCPPLYPGSG--RTDCNER 225
QY 244 LKCKTAETNYCLYWTQVGLNQIKQGGTADATWSKFNKFRREMTLAVLDIIAIPPTVDPE 303
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
226 LKAKIKEYTNYCVGWTKGLDQIQAGTSAEVMKFNKFRREMTLAVLDIIAIPPTVDPE 285
QY 304 KYPLPHTVELTREIYTDVAGSYSGTYSWLRNPNPTFNGLEANGTRGPGVLTWLSKIGIYN 363
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
286 KYPLATSVELTREIYTDVPVYSGGNGYWERFF--SFNSVEANGTRGPGVLTWLAIDIYS 343
QY 364 EYVS---RYFAGWVGTRHYEDYTKNGIFQRMSTGTTSDNLRNIDFQNAVYKITSL---A 417
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
344 HSINLQLGLYSGMGGRHYEDFTKNGAFQRMSTGTTSDNLRNIDFQNAVYKITSLARYA 403
QY 418 INMLVGETTARPEYRVSKADPRVGGPDLYNAGNGLSRMTIESTFPLVLSHNGVR--- 474
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
404 MQPFVGYSI--PRHLVSRABEFPFTLTPLTYEVNMSGYSQ--TIESVLP-----GINKDL 454
QY 475 -----GPHRLSNAACVVYGNRSRVVYGWTHTSKRENIIEANOITQIPAVKSYYLQNYL 529
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
455 PPSRTNYSRLSNAACVQNETSRVNVFGWTHYSMKDKNRIYDPKTIQIPAVKAFALPAGT 514
QY 530 ANAYTVVIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGQSYRIRFRYAADK 588
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
515 GVAGGYVTAGPGYTGDDVTL-----PYQA-----SLKIRLTSAPTNKYRVLRYASGG 564
QY 589 AAFPSVYLYPGWGNRFRVSLKSYSGNYDDLYKSDFKFAEITPPLPSSNIQMDVEMQA 648
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
565 PGFPRVERMSPSSVSN--ANFSRPATGG-----YSSFYVDVTLVTTFNQSGVEIITQN-- 615
QY 649 NSFQSDVNVVLDKIRFLP-----SNTTILEYSGE-----RDLEKTKNAVNDLFTN 693
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
616 ---LSGYHLIVDKVEFIPIDIQIEKCTKQFEGDICRCEGVQSLETKEIVNSLFIN 669
RESULT 6
ADR89435
ID ADR89435 standard; protein; 674 AA.
XX
AC ADR89435;
XX
DT 18-NOV-2004 (first entry)
XX
DE cry24Aa.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.

```

Db 363 VSRYFSGWVGRHYEDYTTGNGNFQMSGTTNDLRDISFPNSDIFPKIESKAIMNLVGEI 422
 Qy 426 TARPEYRSKADFRVGGPDNDYDAGNGLSMTTIESFPVLVHNGVRGP-----SH 478
 Db 423 NARPEYRSABFSSTAFIYLDAGNGLSMTTISKLP-----GKNPSPSYRDYSH 476
 Qy 479 RLSNAACVYVGNVYVGTHTSLKRENIIEANQITQIPAVKSYVLYQWYLANAVTYVIK 538
 Db 477 RLSNAACVAGNSRINIVYVGTHTSMKYNLIYPDKITQIPAKAFDISD---TGPGQVIA 533
 Qy 539 GT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIRPRYAADKAAFFSVLY 597
 Db 534 GPGHTGGNVSL-----PYYSRLKIRLI--PASTKNVLRVRYTSTS-----NGRLL 579
 Qy 598 PGWGSNRVFSLEKSY-----SGNVDDLKYSDFKAEIITPLPSSNQMDVEMQANSFQ 652
 Db 580 VERWSPS-----SIINSFFLPSTGPGDSFGYVD-----TLVTFNQPGVEIILQNL 627
 Qy 653 SDVNVYLDKIEFLPSNTTILEYEGERDLKTKNAVNDLF 691
 Db 628 TPIV--DKVEIPVNSTALEYEGKSLKAEQADVNDLF 664

RESULT 4

ADR89415
 ID ADR89415 standard; protein; 672 AA.

AC ADR89415;

XX 18-NOV-2004 (first entry)

DE AXMI-008.

XX delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.

XX Bacillus thuringiensis.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Encoded by GTC"

XX WO200407462-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

XX 20-FEB-2003; 2003US-0448633P.

XX 20-FEB-2003; 2003US-0448797P.

XX 20-FEB-2003; 2003US-0448806P.

XX 20-FEB-2003; 2003US-0448810P.

XX 20-FEB-2003; 2003US-0448812P.

XX 19-FEB-2004; 2004US-00781979.

XX 19-FEB-2004; 2004US-00782020.

XX 19-FEB-2004; 2004US-00782096.

XX 19-FEB-2004; 2004US-00782141.

XX 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

XX Carozzi N, Hargias T, Koziel MG, Duck NB, Carr B;

XX WPI; 2004-635574/61.

XX N-PSDB; ADR89413, ADR89414.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.

XX Claim 12; SEQ ID NO 27; 178pp; English.
 PS This sequence represents an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX SQ Sequence 672 AA;

Query Match 43.0%; Score 1571.5; DB 8; Length 672;
 Best Local Similarity 47.2%; Pred. No. 2.5e-116;
 Matches 340; Conservative 107; Mismatches 198; Indels 75; Gaps 18;

Qy 1 MKKSPYQNKNEYEILESSNNNTNTPNRYPPANNRDMSTMWDCQGISWDEIWSVETI 60
 Db 1 MKWNSTYQNTNEYELDGSNNNTNNSNRYPPAKDNIPINLDACQGRPWQDTWESVSDI 60
 Qy 61 TSIGINLIEFVIEPSLGGINTLLSIIIGKLIPTNRQTVSALSICDILLSIIRKEVADVSLD 120
 Db 61 VTIGTYLIQLEPGIGGIPVIFSIINKLIPSSGQSVAAALSICDILSVIIRKEVDESVLSD 120
 Qy 121 AIADPDGKLNRYEYLSYLGAWLKDGKPLKTNNSDQGVVYVYKLSERDNEILGSSL 180
 Db 121 GVADPEGEMTAYQDYLYHLEDWLT-----KSNPKLADVVKQFQAREEDFTKLGLAGS 175
 Qy 181 SRNNAQVLLLPFAQAANVQLLLLRDAVOYKAQPPFLSAENVRSELSPNSGCDFTGY 240
 Db 176 SRQAEIILLPTVYQANVHLLLRDAVKYKKEW-----GLVCPPLYPGSG---RTDC 225
 Qy 241 YERLKCTAETNYCLVYVQVGLNQIKQGGTADTWSKFNKFRREMTLAVLDIIAIFPPT 300
 Db 226 NERLKAKIKEYTNYCVGWYNGKLDQIRQAGTSAEWSKFNKFRREMTLAVLDIIAIFPPT 285
 Qy 301 DPEKYPPLTHVELTREIYTDAGVYSSGTYSLRNWPNTPNGLANGTRGPGVLTWLSKIG 360
 Db 286 DFEKYPLATSVELTREIYTDVPGYSGGNYGWERPF--SFNSVEANGTRGPGVLTWLAID 343
 Qy 361 IYNEYVS---RYFAGVGTGRHYEDYTKNGIGIFORMSGTTSDNLRNIDFQNDADVYKITS- 416
 Db 344 IYSHSINQLGYSWGGTGRHYEDFTKNGAFORMSGTTSDNLRNIDFQNDADVYKITS- 403
 Qy 417 --AIMNLVGETTARPEYRSKADFRVGGPDNDYDAGNGLSMTTIESFPVLVHNGVR 474
 Db 404 RYAMQPFVGYSI--PRHLVSRAEFFPTTLNTFLYEVNSSGYSQ-TIESVLP-----GIN 454
 Qy 475 -----GPSHRLSNACVYVGNVYVGTHTSLKRENIIEANQITQIPAVKSYVLYQ 526
 Db 455 KDLPPSRNTNYSRHLNSNAACVQNETSVNVVFGTHTSMKKNRIYDPDKITQIPAVKAFALP 514
 Qy 527 NYLANAVTYVIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIRPRYA 585
 Db 515 AGTVAGGYVTAGPGYTGDDVVTL-----PQA-----SLKRLTSAPTKNRYRLRYA 564
 Qy 586 ADKAAFFSVLYPGWGSNRVFSLEKSYSGNYDDLKYSDFKFAEIIITPLPSSNQMDVE 645
 Db 565 SGGPGPFRVERWSPSSVSN--ANFSRPATGG-----YSSFYVDVTLVTFNQPGVEIILQ 617
 Qy 646 MQANSFQSDVNVLDKIEFLP-----SNTTILEYEG-----RDLEKTKNAVNDLFTN 693
 Db 618 N-----LSGYHLIVDKVEFIPIDIQIEKTKCQPEGDICRCEGVQSLETKKEIVNSLFIN 672

QY 4 MSPYQNKNEYEILESSNNNTNPNRYPFANNRDMSTMWDCOGISWDEIWESVETITSI 63
DB 1 MSPYQNKNEYEILESSNNNTNPNRYPFANNRDMSTMWDCOGISWDEIWESVETITSI 60
QY 64 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIA 123
DB 61 GINLIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIA 120
QY 124 DFGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGQVYFYFKLSERDFNEILGSLSRN 183
DB 121 DFGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGQVYFYFKLSERDFNEILGSLSRN 180
QY 184 NAOVLLPTFAQANVOLLLLRDAVOYKAQWFFPLSAENVRSSELISPNSCDFTGDYIER 243
DB 181 NAOVLLPTFAQANVOLLLLRDAVOYKAQWFFPLSAENVRSSELISPNSCDFTGDYIER 240
QY 244 LKCKTAEYTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTYDFE 303
DB 241 LKCKTAEYTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTYDFE 300
QY 304 KYPLPHVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIGIYN 363
DB 301 KYPLPHVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIGIYN 360
QY 364 EYVSRFAGVGRHYEDYTKNGIFORMSGTTSNDLRNIDFONADVYKITSIAIMNLVG 423
DB 361 EYVSRFAGVGRHYEDYTKNGIFORMSGTTSNDLRNIDFONADVYKITSIAIMNLVG 420
QY 424 ETTARPEYRVSKADFRVGGPDLYDAGNGLSRMTIESTFPLVLHNSVGRGSPSHLSNA 483
DB 421 ETTARPEYRVSKADFRVGGPDLYDAGNGLSRMTIESTFPLVLHNSVGRGSPSHLSNA 480
QY 484 ACVYGNRNVYGVWTHSTLKRNIIEANQITQIPAVKSYLQNYLANAYTYVIKTHGTG 543
DB 481 ACVYGNRNVYGVWTHSTLKRNIIEANQITQIPAVKSYLQNYLANAYTYVIKTHGTG 540
QY 544 GDILRLFKTSEYNAVYAGGIRLIIINNKTAGOSYRIRFRYAADKAAFFSVLYPGWGS 603
DB 541 GDILRLFKTSEYNAVYAGGIRLIIINNKTAGOSYRIRFRYAADKAAFFSVLYPGWGS 600
QY 604 NREVSLEKSYSGNYDDLKYSDFKFABIIPTPLSSNIQMDVEMQANSFQSDVNVVLDKIE 663
DB 601 NREVSLEKSYSGNYDDLKYSDFKFABIIPTPLSSNIQMDVEMQANSFQSDVNVVLDKIE 660
QY 664 FLPSNTTLEYEGERDLEKTKNAVNDLFTN 693
DB 661 FLPSNTTLEYEGERDLEKTKNAVNDLFTN 690

RESULT 3

ADR89439

ID ADR89439 standard; protein; 666 AA.

AC ADR89439;

XX ADR89439;

XX ADR89439;

DT 18-NOV-2004 (first entry)

DE DE

DE DE

KW delta-endotoxin; delta-endotoxin associate polypeptide;

KW expression cassette; transformation; transgenic; plant; bacteria;

KW lepidoptera; coleoptera; pest; pesticide; resistance;

KW pesticidal activity.

XX Bacillus thuringiensis.

XX

XX

PN WO2004074462-A2.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX (ATHE-) ATHENIX CORP.
XX
XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX PT for producing organisms with pesticide resistance.
XX
XX Example 6; SEQ ID NO 51; 178pp; English.
XX
XX This sequence represents a delta-endotoxin crystal protein. This protein
XX was included in the scope of the invention as a comparison to the delta-
XX endotoxins of the invention. Some of the delta-endotoxin coding sequences
XX of the invention have alternative start codons, producing more than one
XX protein from a single open reading frame. The nucleic acid sequences of
XX the invention are useful in DNA constructs or expression cassettes for
XX transformation and expression in plants and bacteria. The nucleic acids
XX and corresponding polypeptides are useful for killing lepidopteran or
XX coleopteran pests. Compositions containing the delta-endotoxins of the
XX invention, and methods for their production, are useful for the
XX production of organisms with pesticide resistance, specifically bacteria
XX and plants. These organisms are useful for generating altered or improved
XX delta-endotoxin or delta-endotoxin-associated proteins that have
XX pesticidal activity, or for detecting the presence of delta-endotoxin or
XX delta-endotoxin-associated proteins or nucleic acids in products or
XX organisms.
XX
XX Sequence 666 AA;

Query Match 63.7%; Score 2329.5; DB 8; Length 666;
Best Local Similarity 67.2%; Pred. No. 6.4e-177;
Matches 470; Conservative 62; Mismatches 116; Indels 51; Gaps 12;

QY 7 YONKNEYEILESSNNNTNPNRYPFANNRDMSTMWDCOGISWDEIWESVETITSIGIN 66
DB 3 YENKNEYEILESSNNNTNPNRYPFANNRDMSTMWDCOGISWDEIWESVETITSIGID 62
QY 67 LIEFVIEPSLGGINTLLSIIGKLIPTNRQTVSALSICDLLSIIRKEVADSVLSDAIADF- 125
DB 63 LIEFLEPSLGGINTLFSIIGKLIPTNHQSVSALSICDLLSIIRKEVADSVLSDAICRFL 122
QY 126 DGKLNRYEYLSYLGAWLKDGPLOKTNNSDIGQVYFYFKLSERDFNEILGSLSRNNA 185
DB 123 DGKLNRYEYLYPYLEAWLKDGPLOKTNNSDIGQVYFYFKLSERDFNEILGSLSRNNA 182
QY 186 QVLLPTFAQANVOLLLLRDAVOYKAQWFFPLSAENVRSSELISPNSCDFTGDYIERLK 245
DB 183 QLLLPYFCACCKCQLLLLRDAVQYEEQWFFPLSAENVRSSELISPNSCDFTGDYIERLK 242
QY 246 CKTAEYTYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAIFPTYDFEY 305
DB 243 CKIAEYTYCEYQAGLNQIKQAGTGADTWSKFNKFRREMTLAVLDIIAIFPTYDFEY 302
QY 306 PLPTHVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIGIYNE 365
DB 303 PLPTHVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLEANGTRGPGLVTLWSKIGIYNE 362
QY 366 VSRFAGVGRHYEDYTKNGIFORMSGTTSNDLRNIDFONADVYKITSIAIMNLVGET 425

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.

PS Claim 12; SEQ ID NO 14; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

XX Sequence 693 AA;

Query Match 100.0%; Score 3655; DB 8; Length 693;
Best Local Similarity 100.0%; Pred. No. 7.6e-283;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKMSPYQKNYEIYELSSNNNTNPNYPFANNRDMSTMWDCQGISWDEIWSVETI 60
DB 1 MKKMSPYQKNYEIYELSSNNNTNPNYPFANNRDMSTMWDCQGISWDEIWSVETI 60
QY 61 TSIGINLIEFVLEPSLGGINTLLSIIIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSD 120
DB 61 TSIGINLIEFVLEPSLGGINTLLSIIIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSD 120
QY 121 AIADFDGKLKNRYEYLSYLGAWLKDGPLOKTNNSDIGQLVYYPKLSERDFNEILGSSL 180
DB 121 AIADFDGKLKNRYEYLSYLGAWLKDGPLOKTNNSDIGQLVYYPKLSERDFNEILGSSL 180
QY 181 SRNNAQVLLPTFAAANVQLLLLRDVAQYKAWPFFLSAENVRSELISPNSGCDFTGDY 240
DB 181 SRNNAQVLLPTFAAANVQLLLLRDVAQYKAWPFFLSAENVRSELISPNSGCDFTGDY 240
QY 241 YERLCKTAETNYCLYQVGLNQLKGGTQADTWSKFNKFRREMTLAVLDIIAIFPT 300
DB 241 YERLCKTAETNYCLYQVGLNQLKGGTQADTWSKFNKFRREMTLAVLDIIAIFPT 300
QY 301 DPEKYPPLPHTVELTREIYTDVAGYSSGTYSWLRNPNFTFNGLEANGTRGPGLVTLWSKIG 360
DB 301 DPEKYPPLPHTVELTREIYTDVAGYSSGTYSWLRNPNFTFNGLEANGTRGPGLVTLWSKIG 360
QY 361 IYNEVYSRPFACWGTGRHYEDYTKNGIFORMSGTSDNLRNIDFQNAVYKITSIAIWN 420
DB 361 IYNEVYSRPFACWGTGRHYEDYTKNGIFORMSGTSDNLRNIDFQNAVYKITSIAIWN 420
QY 421 LVGETTAREYKSVKADPRVGGPDLNVDAGNGLSRMTIESTFPLVHNSGVGPSHRL 480
DB 421 LVGETTAREYKSVKADPRVGGPDLNVDAGNGLSRMTIESTFPLVHNSGVGPSHRL 480
QY 481 SNAACVYVGNRSVNVYVWTHTSKRENIIEANQITQIPAVKSYIYQLNAYTVVIKGT 540
DB 481 SNAACVYVGNRSVNVYVWTHTSKRENIIEANQITQIPAVKSYIYQLNAYTVVIKGT 540
QY 541 HTGGDLIRLRTKSEYNAYAGGRLIINNKTAGQSVIRIRYAADKAAFPVLYPGG 600
DB 541 HTGGDLIRLRTKSEYNAYAGGRLIINNKTAGQSVIRIRYAADKAAFPVLYPGG 600
QY 601 WGSNRFVLSKSYGNDLKYSDFKFARIITPPLPSSNIQMDVMOANSFOSDVNVVLD 660
DB 601 WGSNRFVLSKSYGNDLKYSDFKFARIITPPLPSSNIQMDVMOANSFOSDVNVVLD 660
QY 661 KIEFLPSNTTLEYEGERDLEKTKNAVNDLFTN 693
DB 661 KIEFLPSNTTLEYEGERDLEKTKNAVNDLFTN 693

DB 661 KIEFLPSNTTLEYEGERDLEKTKNAVNDLFTN 693

RESULT 2

ADR89404
ID ADR89404 standard; protein; 690 AA.

AC ADR89404;

DT 18-NOV-2004 (first entry)

DE AXMI-008 alternative protein.

KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.

OS Bacillus thuringiensis.

PN WO2004074462-A2.

PD 02-SEP-2004.

PF 20-FEB-2004; 2004WO-US005829.

PR 20-FEB-2003; 2003US-0448632P.

PR 20-FEB-2003; 2003US-0448633P.

PR 20-FEB-2003; 2003US-0448797P.

PR 20-FEB-2003; 2003US-0448806P.

PR 20-FEB-2003; 2003US-0448810P.

PR 19-FEB-2004; 2004US-00781979.

PR 19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.

PR 19-FEB-2004; 2004US-00782141.

PR 19-FEB-2004; 2004US-00782570.

PR 19-FEB-2004; 2004US-00783417.

XX (ATHE-) ATHENIX CORP.

PA Carozzi N, Hargliss T, Koziel MG, Duck NB, Carr B;

PI WPI; 2004-635574/61.

DR N-PSDB; ADR89403.

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
XX for producing organisms with pesticide resistance.

PS Claim 12; SEQ ID NO 16; 178pp; English.

XX This sequence represents an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

SQ Sequence 690 AA;

Query Match 99.6%; Score 3640; DB 8; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.2e-281;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2005, 11:07:19 ; Search time 190 Seconds
(without alignments)
1602.576 Million cell updates/sec

Title: US-10-781-979-3

Perfect score: 3655

Sequence: 1 MKQMSPYQNKVEVLELSSS.....YEGERDLEKTKVAVNDLFTN 693

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3655	100.0	693	ADR89402	Adr89402 AXMI-008.
2	3640	99.6	690	ADR89404	Adr89404 AXMI-008
3	2329.5	63.7	666	ADR89439	Adr89439 cry40Aa1.
4	1571.5	43.0	672	ADR89415	Adr89415 AXMI-008.
5	1561.5	42.7	669	ADR89417	Adr89417 AXMI-008
6	831	22.7	674	ADR89435	Adr89435 cry24Aa.
7	747	20.4	1151	Aea81457	Aea81457 Bacillus
8	747	20.4	1156	AAW46856	AAW46856 Bacillus
9	747	20.4	1156	AAy24959	AAy24959 Bacillus
10	747	20.4	1156	AEA81456	AEA81456 Bacillus
11	747	20.4	1279	AAy82988	AAy82988 Native Cr
12	745	20.4	1169	AAW06417	AAW06417 Antiscara
13	728.5	19.9	704	AAK51693	AAK51693 B.thuring
14	728.5	19.9	1149	AAK32354	AAK32354 Coleopter
15	728.5	19.9	1149	AAK51692	AAK51692 B.thuring
16	725	19.8	1167	AAU80281	AAU80281 Bacillus
17	724	19.8	659	ADR89437	Adr89437 cry39Aa.
18	724	19.8	1208	AAU02093	AAU02093 Bacillus
19	713.5	19.5	1206	AAU99255	AAU99255 Bacillus
20	713.5	19.5	1206	ADL15305	ADL15305 B.thuring
21	713.5	19.5	1206	AEA45607	AEA45607 B. thurin
22	712	19.5	802	AAU02035	AAU02035 B. thurin
23	708.5	19.4	1227	AAV31990	AAV31990 Chimeric
24	707.5	19.4	719	ABB07073	ABB07073 Bacillus

25	707.5	19.4	719	9	ADY59880	Ady59880 Bacillus
26	707.5	19.4	719	9	ADY59881	Ady59881 Bacillus
27	705.5	19.3	1209	4	AAU02094	AAU02094 Bacillus
28	705.5	19.3	1228	9	ADY59858	Ady59858 Bacillus
29	703.5	19.2	652	3	AAy83039	AAy83039 Cry9Aa to
30	703.5	19.2	656	3	AAy83040	AAy83040 Synthesis
31	702.5	19.2	1228	2	AAK50955	AAK50955 Bacillus
32	700	19.2	710	4	AAU02041	AAU02041 B. thurin
33	699	19.1	1217	4	AAU02092	AAU02092 Bacillus
34	690.5	18.9	675	8	ADR89436	Adr89436 cry25Aa.
35	689	18.9	1227	2	AAW44321	AAW44321 Bacillus
36	689	18.9	1227	4	AAK19950	AAK19950 Bacillus
37	686	18.8	1227	4	AAU02046	AAU02046 B. thurin
38	683	18.7	682	8	ADR89408	Adr89408 AXMI-009.
39	681	18.6	1186	2	AAy16796	AAy16796 Amino aci
40	681	18.6	1230	8	ADK98484	Adk98484 B thuring
41	681	18.6	1230	8	ADK98489	Adk98489 B thuring
42	681	18.6	1230	8	ADK98481	Adk98481 B thuring
43	681	18.6	1230	8	ADK98491	Adk98491 B thuring
44	681	18.6	1230	8	ADK98487	Adk98487 B thuring
45	679	18.6	719	4	AAK66908	AAK66908 Insectici

ALIGNMENTS

RESULT 1
ADR89402
ID ADR89402 standard; protein; 693 AA.
AC ADR89402;
XX
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008.
XX
KW delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by GTG"
XX
XX WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
XX 20-FEB-2003; 2003US-0448633P.
XX 20-FEB-2003; 2003US-0448797P.
XX 20-FEB-2003; 2003US-0448806P.
XX 20-FEB-2003; 2003US-0448810P.
XX 20-FEB-2003; 2003US-0448812P.
XX 19-FEB-2004; 2004US-00781979.
XX 19-FEB-2004; 2004US-00782020.
XX 19-FEB-2004; 2004US-00782096.
XX 19-FEB-2004; 2004US-00782141.
XX 19-FEB-2004; 2004US-00782570.
XX 19-FEB-2004; 2004US-00783417.
XX (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
WPI; 2004-635574/61.
XX N-PSDB; ADR89400, ADR89401.

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RESULT 14

```
Db 448 QLODSENELPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHSADRTNTINSDSI 507
Qy 515 TQIPAVKSYLQNYLANAYTVIKGT-HTGGDLIRFLRTKSEYNNAVAGGIRLIINKKT 573
Db 508 TQIPLVKAFNLPSSGAS-----VVRGPGFTGGDILQRTNTGT-----FGDIRVNIINPPF 555
Qy 574 AGQSYRIRFRYAADKAAFFSVLYPGGWSNRFSVLSKSYSGNY-----DOLKYDFK 626
Db 556 A-QRYLRIRYASNTNLEFHTSI--NGKAINQ-----GNFSATMNRGDDLDYKAFR 603
Qy 627 FAETIITPLPSSNQMDVEMQANSFQSDVNVVLDKIEFLPSNTTTLLEYEGERDLEKTKNA 686
Db 604 TVG-FTTFFSFSNAQSTFTIGANNFSLGNEVYIDRIEFVPEVT---YEAYDLKKAQDE 659
Qy 687 VNDLFTN 693
Db 660 ITAMFTS 666
```

RESULT 12

```
CRIBA_BACTK STANDARD; PRT; 1228 AA.
ID POA373; P05517; Q45731;
AC 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cryIaB (insecticidal delta-endotoxin
DE CryIaB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Names=cryIaB; Synonyms=cryA4, cryIaB(a);
OS Bacillus thuringiensis subsp. kurstaki.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=29339;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
CC -I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
```

```
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
```

```
CC -----
CC EMBL; X06711; CAA29898.1; -; Genomic_DNA.
DR PIR; S00873; S00873.
DR HSSP; P07130; 1DLCL.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
SQ SEQUENCE 1228 AA; 139648 MW; C8E3A19FB5D98575 CRC64;
```

```
Query Match 19.3%; Score 705.5; DB 1; Length 1228;
Best Local Similarity 31.3%; Pred. No. 4.8e-40;
Matches 224; Conservative 118; Mismatches 279; Indels 95; Gaps 31;
```

```
Qy 10 KNEVEILESSNNTTNPYPFANNRDMSTMNDQGISWDEIWSVEVITISGINLIE 69
Db 6 KNENELINAVNSHSAQMDLLPDARIEDSLCIA-----EGNNIDP-FVSASTVQT-GINIAG 59
Qy 70 FVI-----EPSLGGINTLLS-IIGKLIPTNRQTVSALSICDLSIIRKEVADSVLSDAIAD 124
Db 60 RIILGVLPAGQALSAFYSFLVGLWPRGDDQWE-IFLEHVEQLINQOITENARNTALAR 118
Qy 125 FDGKLNRYEYLYSILGAWLKDGKPLQKTNNSDIGOLVY--YFKLSERDFNEILGGLSLR 182
Db 119 LQGLGDSFRAYQOS-LEDW-----LENRDARTSRVLYTQYIAL-ELDFLNAMPLFAIR 170
Qy 183 NNAQVLLLTPTFAQAAVQILLIRDAVQYKAOFPFLSAENVRSELISPNCGCFTGYE 242
Db 171 NQ-EVPLLMVYAAANLHLLLRDASLFGSE-FGLTSQEIQR-----YYE 213
Qy 243 RLKCKTAETNYCLYVYQVGLNOIKQGGTADTWSKFNKPRRREMTLAVLDIIAIFPTYDF 302
Db 214 RQVERTRDYSDYCVIEWYNTGLNSLR--GTNAASWVYVYVQRRDLTLGLVLDVALFSDYDT 271
Qy 303 EKYPLPETHVELTREIYTDV--GYSSGTYSMLRNMPNTFNGLEANGTRGPGVLVTWLSKI 359
Db 272 RTYPINTSAQLTREYVYDAIGATGVNMAWNNWNNNAPSFAEAAAIRSPHLLDFLEQL 331
Qy 360 GIYNEVSYRYFAGWVGRHYEDYTKNGIFORMSG-----TTSNDLRNIDPQNA 408
Db 332 TIFSA-----SSRWSNTRHM-TYWRGHTIOSRPIGGGLNTSTHGATNTSINPVTLPASR 385
Qy 409 DVYKITSLAIMLVGTTARTARPEYRVSKAOPRRVGGPDLNVDAG-----NNGLSRMT 459
Db 386 DYTRESYAGVLLWG-IYLEPIHGVTVPFNFNPQNIS-DRGTANYSPYESPGQLQKD 443
Qy 460 IESTF-PLVLHNGVRGSPSHLSNAACVYVYGVNSRVNYGWTHTSLKRENIIEANQITQIP 518
Db 444 SETLEPPETTERPNYESYSHRLSHIGIILQSRVNVVPVYSWTHRSADRTNTIGPNRITQIP 503
Qy 519 AVKSYLQNYLANAYTVIKGT-HTGGDLIRFLRTKSEYNNAVAGGIRLIINKTAGQS 577
Db 504 MYKASELPQ-----GTVVVRGPGFTGGDILR--RTNTG-----GFGPIRVTVNGPLT-QR 550
Qy 578 YRIRFRYAADKAAFFSVLYPGGWSNRFSVLSKSYSGNYDLYKSDPKFAEIIITPLPS 637
Db 551 YRIGFRYAS--TVDFDFVSRGGTVVNNRFRFRTNWSG--DELYGNF-VRRFTTPTFTF 605
Qy 638 SNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTTLLEYEGERDLEKTKNAVNDLFTN 693
Db 606 TQIQDIIRTSIQGLSGNGEVYIDKIEIP---VTATFEAYDLERAQEAVALFTN 658
```

RESULT 13

```
Q93NM5 BACTU PRELIMINARY; PRT; 1228 AA.
ID Q93NM5;
AC Q93NM5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry1Ba.
GN Name=cry1Ba;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang J., Song F., Huang D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF368257; AAK63251.1; -; Genomic_DNA.
DR HSSP; P07130; 1DLCL.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
```

```
DR Pfam: PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1144 AA; 128060 MW; 98F93070C49014AB CRC64;

Query Match
Best Local Similarity 19.4%; Score 709; DB 2; Length 1144;
Matches 234; Conservative 123; Mismatches 266; Indels 126; Gaps 35;

QY 4 MSPYQNKNEYELLESSNNNTNPN--RYPFANNR--DMSTMSWNCQGISW---DEIWES 56
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 59
QY 57 VETITS-----IGINLIEFV----EPLSGGINLTLIS-IIGKLIPTRQTVSALSICDLL 106
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 109
QY 60 PETFISSTVQTGIGIVGVGALGVPPAGQIASFYFVIGQLWPSSTVSVMEMKQVE 119
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 122
QY 107 SIIRKEVADSVLSDAIDPDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDI---GQLVY 163
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 166
QY 120 DLIDQKITDSVRKTAGLQGG-LGDLGVYQKSLKNWLE-----NRNDTRARSVVVT 170
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 173
QY 164 YFKLSRDENEILGSSLSRNNAQVLLPTFAQAAVQVLLLRDVAQYKAQWPFPLSAENV 223
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 226
QY 171 QYIALELDFVAKI-PFSAISGGQVPLLSVYAQAANLHLLLRDASIFGAEW-GFTTGE-- 226
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 229
QY 224 RSELISPNSGCDFTGDYERLCKTAETNYCLYVYQVGLNQIKOGGTGADTWSKFNKPR 283
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 286
QY 227 -----ISTFYDQVTRTAQYSDYCVKWNVTGLDKL-GTNAASWLKXHQPR 271
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 274
QY 284 REMTLAVLDIIAIFPYDEKYPPLPHTVELTREIYDVGY---SSGTY--SWLRNWPNT 338
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 341
QY 272 REMTLVLVDLALFNPYDRTYPIETTAQLTREVTDPVFNRETSGGFCRRWSLNSDIS 331
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 334
QY 339 ENGLRANGVRGCLVTLWSKIGLYNEV-----SRYPAGWVGRHYEDYTKNGIFQRM 392
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 395
QY 332 FSEVESAVIRSHPLFDLSEIFYTTRAGLPLNNTLEYVWGHISIKYKNTNASSALERN 391
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 394
QY 393 SGT-TSNDLRNIDFQADYVYKITSLA--IMNLVGETTARPEYRVSKADPRRVGGPDLYD 449
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 452
QY 392 YGTITSNKIKYVLDANKDIFQVRSGLADLANIYAQV-----YGVVYASFTLL--DKNTG 443
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 446
QY 450 AGN-NGLSRMTIESTPPLVHLNGV-----RQPSHRLS-----NAACV 487
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 490
QY 444 SGSVGFTYSKPHITMQVCTQNYNTTIDEIPPEPLSRGYSHRLSHITSYSPSKNASSPA 503
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 506
QY 488 -YGNRVNVYVGHVTHSLKRENIIEANQITQIPAVKSYVLQYLANAYTVVIKGT-HTGCD 545
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 548
QY 504 RYGN--LPVFWATHRADVTNIVYSDKITQIPVWKAHTLV-----SGTIVIKGPGFTGN 556
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 559
QY 546 LIRFLRTKS---EYNAVYAGGGIRLIINNKTAGQSVYRIRFRYAADKAAPFVYLYPGGW 602
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 605
QY 557 ILK--RTSSGPLAYTSVSV-----KSPLSQRYRARIYASTTNLRLFTVI-----S 600
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 603
QY 603 SNRFVLSKYSNGY--DDLKYSDFKFAEIIITPLPSSNTQMDEVQANSFQSDVNVLDK 661
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 664
QY 601 GTRIYSINVNTKMTNKGDDLTFTFDLATIGT-AFTFSNYSDSLTVGADSFASGGEVYDK 659
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 662
QY 662 IEPFSPNTTLEYEGERDLKTKNAVNDL 690
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 693
QY 660 FELIPVNAI---FEAEEDLDVAKKAVKNL 685
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 688

RESULT 11
CR1ID BACTU
ID CR1ID BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal protein cryII(d) (Insecticidal delta-endotoxin
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name-cryIId; Synonyms=cryIId), NrcryI;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
```

```
Qy 386 NGIFORMSGTTSNDLRNIDFONADVYKI-----TSLAIMNLVGETTAR 428
Db 386 SS-FNKYSGLVAGAEIIPVQNDIYRVVWTYIGRYNSLLGVNPNVTFYFSNNTQKTYSK 444
Qy 429 PEY---RVSKADFRRVGGPDL---NYDAGNGLSRMT---IESTFPLVLHNSGVGRGSHR 479
Db 445 PKQFAGGIKTID---SGBELTYENQSYSHRVSITYTSFEIKSTGGTVL---GV----- 491
Qy 480 LSNACVVYGNRNVVYGTHTSLKRENIIEANOITQIPAVKSYLYQLVNLAYTVYVIK 539
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVWNFOEG 535
Qy 540 THTGGDLIRLRTKSEYNNAVAGG-----IRLIINNKTAGOSYRIRFRYAADKAAPFSV 594
Db 536 LYNGGPMVKL-----SGSGSQVINLRVATDAKGASQRYRIRIRYASDRAGKFTI 584
Qy 595 YLPGGWSNRVFSLEKSYSGNY-----DDLKYSDFKPAEIIPTPLPSSNIQMDVE 645
Db 585 -----SSRSPENPATYSASIAYTNTMSTNASLTYSTFAYAE-----SGPINLGIS 629
Qy 646 MQANSFQSDV-----NVVLDKIEPLPSNTTILEYEGERDLEKTKNAVNDLFTN 693
Db 630 GSSRTFDISITKEAGANLYIDRIEFIPVNTL---FEAEDLDVAKAVNGLFTN 681
```

RESULT 9

```
Q6R2R6_BACTU
ID Q6R2R6_BACTU PRELIMINARY; PRT; 1160 AA.
AC Q6R2R6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE HBF-1 CryIII delta-endotoxin.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID=1428;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song F., Zhu C., Zhang J.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY518201; AAR98783.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF03945; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1160 AA; 130452 MW; C794F99AD1397188 CRC64;
```

```
Query Match 19.9%; Score 728.5; DB 2; Length 1160;
Best Local Similarity 29.9%; Pred. NO. 1.1e-41;
Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;

Qy 4 MSPYQNKNEYEILSSNNNTNTPN--RYPPANNRDMSTMSWNCQGISWDE----- 52
Db 1 MSP-NKNEYEIIIDALSPVSNSIRYPLANDQNTWLNQMYKYDKLKTSTNAELSRN 59
Qy 53 --IWSEVETITSGINLIEFVIE---PSLGGINTLL-SIIGKLIPTNRQTYSALSICDL 105
Db 60 PGTFISAQAVGTDIVSTIISGLGIPVLGEVFSILGSLIGLLWPSNNENWQIFMNRV 119
Qy 106 LSIIRKEVADSVLSDAIAFDGKLKNYR---EYILSYLGAWLKDGKPLQKTNNSIGQVL 162
Db 120 BELIDQKILDSVRSRAID----LANSRIAVEYQNALEDWRKNP---HSTRSAAL---- 168
Qy 163 YYPKLSERDFN--EILG---GSLSRNNAOVLLLPTEFAQANVOLLLLRDAVOYKQWPF 217
```

```
Db 169 -----VKERFGNAEAILRNMGSPSQNTYETPLPTTAAQAASLHLLVNRDVQIYCKEWG-- 222
Qy 218 LSAENVRSELISPNSCDFTGDYERLCKTAETYNCLYVYQVGLNQIKQGGTGADTWS 277
Db 223 -----YQNDIDL---PYKEQVSYTARYSDHCQVQYNAGLNKLR--GTGAKQWV 266
Qy 278 KFNKPREMTLAVLDIAIAPFTYDFEKYPLPHTVELTREIYTDVAG--YSSGTSWLNRP 336
Db 267 DYNRFRERVMVYLDVALFPNDYDARIYPLETNAELTREIFDPVGSYVTVGQSSTLISY 326
Qy 337 N-----TFNGLEANGTRGPGLVTLWSKIGIYNEY-----VSRVFAAGWCTRHYEDVTGK 385
Db 327 DMIPALPSESTLE-NLLAKPDPFTLLQIRMYTSFRONGTIEYYNWGGQRLTSLIYG 385
Qy 386 NGIFORMSGTTSNDLRNIDFONADVYKI-----TSLAIMNLVGETTAR 428
Db 386 SS-FNKYSGLVAGAEIIPVQNDIYRVVWTYIGRYNSLLGVNPNVTFYFSNNTQKTYSK 444
Qy 429 PEY---RVSKADFRRVGGPDL---NYDAGNGLSRMT---IESTFPLVLHNSGVGRGSHR 479
Db 445 PKQFAGGIKTID---SGBELTYENQSYSHRVSITYTSFEIKSTGGTVL---GV----- 491
Qy 480 LSNACVVYGNRNVVYGTHTSLKRENIIEANOITQIPAVKSYLYQLVNLAYTVYVIK 539
Db 492 -----VPIFGWTHSSASRNNFIYATKISQIPINKA---SRTSGGAVWNFOEG 535
Qy 540 THTGGDLIRLRTKSEYNNAVAGG-----IRLIINNKTAGOSYRIRFRYAADKAAPFSV 594
Db 536 LYNGGPMVKL-----SGSGSQVINLRVATDAKGASQRYRIRIRYASDRAGKFTI 584
Qy 595 YLPGGWSNRVFSLEKSYSGNY-----DDLKYSDFKPAEIIPTPLPSSNIQMDVE 645
Db 585 -----SSRSPENPATYSASIAYTNTMSTNASLTYSTFAYAE-----SGPINLGIS 629
Qy 646 MQANSFQSDV-----NVVLDKIEPLPSNTTILEYEGERDLEKTKNAVNDLFTN 693
Db 630 GSSRTFDISITKEAGANLYIDRIEFIPVNTL---FEAEDLDVAKAVNGLFTN 681
```

RESULT 10

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Q8KZL7_BACTG
ID Q8KZL7_BACTG PRELIMINARY; PRT; 1144 AA.
AC Q8KZL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cry8 protein.
GN Name=Cry8;
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=29338;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SDS-502;
RA Asano S., Yamashita C., Iizuka T., Takeuchi K., Yamanaka S., Cerf D.,
RA Yamamoto T.;
RT "A strain of Bacillus thuringiensis subsp. galleriae containing a
RT novel cry8 gene highly toxic to Anomala cuprea (Coleoptera:
RT Scarabaeidae).";
RL Biol. Control 28:191-196(2003).
DR EMBL; AB089299; BAC07226.1; -; Genomic DNA.
DR HSSP; Q06117; 1J16.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
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Db 1 MNSYENKNEVEILLNDKSKNSMNPYLRYPFLANDSLASMQNTNYKD-----WLTMCDDRTDT 55
Qy 60 --ITSIGINLIEFVIEPSGGTLLSIIGKLIPTNRQTVSAL-----100
Db 56 DVLSSRG-----AVSTGVGLSTILSLFG--IPLIGEGIDILLGAADFLWPESDGHQY 107
Qy 101 STCDLLSIIRKEVADSVL-----SDAIDPDGKLNRYEYLSYLGAWLKD--GKPLQKTN 154
Db 108 TWEDLNWHI--EELMDERLETERKTALDRLG--LKALLGLFRDAPDSWEKQNDPIAKNR 165
Qy 155 NSDIGOLVYVYKLSERDFNEILGSLSRNNAQVLLLPFAQANVQLLLRDVAQYKQW 214
Db 166 ---VGG---YFEDVHTHFVKDMASIPSATNYEVLPLPVYAQAANLHLLLRREGVLYGSRW 219
Qy 215 FFLSNAENRSELISPSNCDTGDYERLCKTAYTNYCLYVQVGLNQIKQGGTGAD 274
Db 220 G-----IAP--AADF---YHDQLLYTAIYANHCVTYWYNNGLAQOQKELFAKSP 262
Qy 275 TWSKFNKFRREMTLAVLDIIAIFPTDYFEKYPLPHTHVELTREIYTDVAGYSSGTYSWLRN 334
Db 263 NNRNFNAYRDMTITVLDIIAIFPTDYDARLYKPKTELTRIEYSDVNLND--VTGVQO- 319
Qy 335 WPNFTNGLANGTRGPGLVTLWLSKIGIYNEYRSYFAGWVGRHYEDYTKGNGIFQIMS- 393
Db 320 --TDLNKNEAFTSRPHLVRLRGDFDYTRTKYAYWRYLAGHTNYFSFT--GNGTIYSSSF 376
Qy 394 -----GTTSDNLRNIDFQNAVYKITSIAIMLVGETTARPEYRVSKADPRVGGDPLN 447
Db 377 NNWYDTMTKSTINIPDY--ANIYKLWTKSYTNISPYT---DPVGISQMQFSLTNQOULT 431
Qy 448 YDAGNNGLSRMWTSTF-----PLVLHNGVRGSPSHRLS--NAACVVYGNRVN-VY 496
Db 432 YT--GTSAPKYPVRETFEIPPTDEKPLIYENY-----SHLSYMTSAHQFGDKKIGYTF 484
Qy 497 GWTHTSLKRENTIEANQITQIPAVKSYLLQNYLANAYTVYIKGT--HTGGDLIRFLRTKSE 555
Db 485 AMWHSVDPNRVDPKITQIPAVKGYLQ-----YGVYKQPGHGTGDLVSMIRTD-- 536
Qy 556 YNAVAGGIRLIIN-NKTAGOSYRIRFYADKAFFSVLYPGWGSNRFVSLEKSY- 613
Db 537 -----RGINVYFPQPLDYRIRIRYSTSNGY--LYTYS---PNTKIVILPPTTL 581
Qy 614 ---SGNYDLYKSDKFAEIIPTPLPSSNIQMDVEMQANSFQSDV-----NV 657
Db 582 VDGQPTFDPMDSAFRVZV-----PA-----SFRASVAGYNTFTIEAGFGPV 624
Qy 658 VLDKIEFLPSNTTTLLEYEGERDLEKTKNAVNDLFTN 693
Db 625 YIDKIEFIPDNTTTLLEYEGGRDLEKTKNAVNDLFTN 660

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RESULT 8

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CRCA_BACTP STANDARD; PRT; 1160 AA.
ID CRCA_BACTP
AC Q45706;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE Pesticidal crystal protein cry8Ca (insecticidal delta-endotoxin
DE CryVIIIc(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry8Ca; Synonyms=cryIII, cryVIIIc(a);
OS Bacillus thuringiensis subsp. japonensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxId=128936;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Buibui.
RX MEDLINE=94100786; PubMed=7764305;
RA Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N.,
RA Hori H., Asano S., Ohba M., Iwahana H.;

```

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RT "Cloning, heterologous expression, and localization of a novel crystal
RT protein gene from Bacillus thuringiensis serovar japonensis strain
RT buibui toxic to scarabaeid insects.";
RL Curr. Microbiol. 28:15-19(1994).
RN [2]
RP PROTEIN SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.
RX MEDLINE=94259659; PubMed=8200856;
RA Hori H., Suzuki N., Ogiwara K., Himejima M., Indrasith L.S.,
RA Minami M., Asano S., Sato R., Ohba M., Iwahana H.;
RT "Characterization of larvicidal toxin protein from Bacillus
RT thuringiensis serovar japonensis strain Buibui specific for scarabaeid
RT beetles.";
RL J. Appl. Bacteriol. 76:307-313(1994).
CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of insects. Active on various scarabaeid beetles
CC such as Anomala cuprea, A. rufocuprea and Popillia japonica.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U04366; AAA21119.1; -; Genomic_DNA.
DR PIR; 140589; 140589.
DR HSP; Q06117; 1J16.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
KW Direct protein sequencing; Sporulation; Toxin.
SQ SEQUENCE 1160 AA; 130426 MW; C16C3D912BEB751 CRC64;

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Query Match 19.9%; Score 728.5; DB 1; Length 1160;
Best Local Similarity 29.9%; Pred. No. 1.1e-41;
Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;
Qy 4 MSPQNKNEYEILSSSNNTNTPN--RYFPANRDMSTMWNSDCGISWDE-----52
Db 1 MSP--NNQNEYEIIIDALSPTSVDNSIRYPLANDQNTLQNNMYKDYLKWTSTNAELSRN 59
Qy 53 --IWESVETITISIGINLIEFVIE---PSLGGINTLL--SIIGKLIPTNRQTVSALSICDL 105
Db 60 PGTISAQDAGVTGIDIVSTIISGLGIPVLGEVFSILGSLIGLWPSNNVWQIFMNRV 119
Qy 106 LSIIRKEVADSVLSDAIDPDGKLNRYR---EYLSYLGAWLKDQKPLQKTNNSDQGLV 162
Db 120 EELIDQKILDSVRSRAID-----LANSRIAYEYQNALEDWRKNP---HSTRSAAL-----168
Qy 163 YFFKLSERDFN--BILG---GSLSRNNAQVLLLPFAQANVQLLLRDVAQYKQWPPF 217
Db 169 ---VKERFGNAEAILRNTMGSPSQTNVETPLPPTYAQAASLHLLVMDVQIYKKEW- 222
Qy 218 LSAENVRSELISPSNGCDFTGDYERLCKTAYTNYCLYVQVGLNQIKQGGTGADTWS 277
Db 223 -----YPQNDIDL-----FYKQSVSYTARYSDHCQVYNAGLNKLR--GTGAKQWV 266
Qy 278 KFNKFRREMTLAVLDIIAIFPTDYFEKYPLPHTHVELTREIYTDVAGYSSGTYSWLRNP 336
Db 267 DYNRFRREMNWVLDLVALFPNYDARIYPLTNAELTREIFTDPVGSVVTGSSSTLSWY 326
Qy 337 N-----TFNGLEANGTRGPGLVTLWLSKIGIYNEY-----VSRYFAGWVGRHYEDYTKG 385
Db 327 DMIPALPSPFSTLE-NLLRKDPFTLLQELIRMYTSFRQNGTIEYNYWGGQRLTSLYIYG 385

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RESULT 6
CR8BA_BACUK STANDARD; PRT; 1169 AA.
ID CR8BA_BACUK
AC Q45705;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pepticidal crystal protein cry8Ba (insecticidal delta-endotoxin
DE Protein) (Crystalline entomocidal protoxin) (134 kDa crystal
DE protein).
GN Name=cry8Ba; Synonyms=50C(b), cryVIIIb(a);
OS Bacillus thuringiensis subsp. kumamotoensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=132267;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=NRRL B-18746 / PS50C;
RA Michaels T.E., Foncerrada L., Narva K.E.;
RT "Process for controlling scarab pests with Bacillus thuringiensis
RT isolates.";
RL Patent number WO93115206, 05-AUG-1993.
CC -I- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of insects. Active on various scarabaeid beetles.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U04365; AAA21118.1; -; Genomic_DNA.
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Sporulation; Toxin.
DR KW Sporulation; Toxin.
DR SEQUENCE 1169 AA; 133544 MW; 22EEFCF5BD699909 CRC64;

Query Match 20.4%; Score 745; DB 1; Length 1169;
Best Local Similarity 29.4%; Pred. No. 7.9e-43;
Matches 217; Conservative 142; Mismatches 274; Indels 104; Gaps 31;

QY 4 MSPYQNKNEYEILES--SSNTNTNRYPPAN--NRDMSTMSWDCQGIS-----W 50
DB 1 MSP-NQNEYEIIIDATPSTSVSDNSRYPFANEPTNALQNDYKYLKMSAGNVSEYPOS 59
QY 51 DEIWESVETITSGINLIEFVIE-----PSLGGINTLLS-IIGKLIPTNRQTVSALSICDL 105
DB 60 PEVFLSEQDAVKAADIIVGKLLTGLGVFPVGPVSLVTLQIDILWPSKQSQWEIFMEQV 119
QY 106 LSIIRKEVADSVLSDAIAPDGKLNKYREYLSYLGAWKD---GKPLKTNNSDIGQVL 162
DB 120 EELINQKIAEYANKALSELEGGINNY-QLYLTALSEWKENPNNGSRALRDVNR----- 172
QY 163 YVFKLSERDFNEITLGGSLRNNAQVLLPTFAQANVQLLLLRDAVQYKAQMPFLSAEN 222
DB 173 --FEILDSLFTQYM-PSFRVTNFEVFLTYTWAANLHLLLRDASIFGEW--GLUSTST 227
QY 223 YRELISPNSGCDFTGDYERLCKTAETNYCLYQVGLNQIKGGTGADTWSKFNKF 282
DB 228 I-----NNYNRQMKLTAEYSDHCVKWYETGLAKLK--GSSAKQWIDYNQF 271

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283 RREMTLAVLDIIAIPFYDFEYKPLTHVELTREIYTDVAGYSS--GTYSWLRNWPNTFN 340
272 RREMTLTVLDDVALFSNYDTRTYPLATTQAQLTREYVTDPLGAVDVPNIGSWYDKAP-SFS 330
341 GLEANGTRGPGVLTWLSKIGIYNEYVS---RYFAGWVGTRHRYEDVTGKNGIFQMSGTT 396
331 EIEKAIRPHPHVDYITGLTVYTKRSFTSDRYMRWAGHOISYKHIGTSSTTQMYGTN 390
397 SN--DLNRNIDFQNAVYKITS--LAIMNLVGETTARPEYRVSKADFRVVG-----GPDLN 447
391 QNLQSTNFDFTNYDIYKTLNSGAVLDDIVYPGYTVTFGMPETEFPMVNLNTRKTLT 450
448 YDAGNNGLSRMITESTFPLVLSNG---VRGSHRLSNAACVYVGNR---VVVYGWHTHT 501
451 YKPASKDIIIDTRDSELEPPTSGQPNYESYSHRLGHIT-FIYSSSTSTYVPVFSWTHR 509
502 SLKRENIIEANOITQIPAVKSYVLYQLYANAVTYVIKGT-HTGGDLIRFLRT--KSYNA 558
510 SADLTNVTKSGEITQIPGKSSTI-----GRNTYIIKRGYTGCDLVALTDTRIGSCFQM 564
559 VYAGGIRLIINNKTAGQSYRIRFRYADKAAFFSVLYPGMGWSNRFSVLSKSYSG-NY 617
565 IF-----PESQRFIRIRYASNETSYISLY---GLNQSGTLKFNQYTSNKNE 608
618 DDLKYSDPKFALIPPLPSSNIQMDVEMQANSFQSDVNV-VLDKIEPLPSNTTLEYEG 676
609 NDLTYNDFKYEY--PRVISVNASSNIQRLSIGIQTNTNLFLIDRIEFPVDET---YEA 663
677 ERDLEKTKNAVNDLFTN 693
664 ETDLEAKKAVNALFTN 680

RESULT 7
Q8RQU6_BACTA PRELIMINARY; PRT; 660 AA.
ID Q8RQU6_BACTA
AC Q8RQU6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mosquitocidal toxin (fragment).
GN Name=cry39A;
OS Bacillus thuringiensis (subsp. aizawai).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1433;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ito T., Sahara K., Bando H., Asano S.;
RT "Cloning and Expression of Novel Crystal Protein Genes cry39A and
RT 39orf2 from Bacillus thuringiensis subsp. aizawai Buni-14 Encoding
RT Mosquitocidal Proteins.";
RL J. Insect Biotechnol. Sericulture 71:123-128 (2002).
DR EMBL; AB074413; BAB72016.2; -; Genomic_DNA.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR NON_TER 1
FT SEQUENCE 660 AA; 75643 MW; A92EF6257C2B9404 CRC64;

Query Match 19.9%; Score 729; DB 2; Length 660;
Best Local Similarity 31.5%; Pred. No. 4.8e-42;
Matches 238; Conservative 106; Mismatches 250; Indels 162; Gaps 37;

QY 4 MSPYQNKNEYEILES--SSNTNTNRYPPAN--RDMSTMSWDCQGISWDEIWESVET 59

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Db 392 PITNIRDNDIYKVDLAAAYVATIRNALDST-----FGVSSSHFFNNMGKNLYQS-KQPY 445
 QY 456 SRMTTESTPLVLHNG-VRGPSHRLSNAACV-----VYGNRVVNYGTHHTSLKRE 506
 Db 446 PYPITITPGRESLEGNVDYSHLLCNVKNITGGLRQTSARGSLSLSHAWTHKSLNPK 505
 QY 507 NIIEANQITQIPAVKSYLYQLANAYTYVIKGT-HTCGDLIRFLRTKSEYNAVYAGGI 565
 Db 506 NIIAADKITHIPAVKSNL-----SASSAVIKPGFTGGDLR-LGPNOFVDYI----- 553
 QY 566 RLIIINKTAGQSY-RIRFRYADKAFFSVYLYPGGWSNRVSLK-KSYSGNYDDLKYS 623
 Db 554 -LTPDNPQVSYFYDRLRYACMGGANILIQF-----WNKNWIGVQLVSTTSLENLKYE 608
 QY 624 DFKFABIIPTPLSSNIQMDVMOANSFOSDVNVLDKIEFLPSNTTILEYEGERDLEKT 683
 Db 609 NFAY-----ITRLSFTFGQGYNMYSINPTSNENVIIDKIEFLPVSGTPPEYEGKHLKNT 665
 QY 684 KNAVNDLFTN 693
 Db 666 QADVNNLFLN 675

RESULT 5

CR9AA_BACTG
 ID CR9AA_BACTG STANDARD; PRT; 1156 AA.
 AC Q9031; Q03747;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Pestidical crystal protein cry9Aa precursor (insecticidal delta-endotoxin CryIXA(a)) (Crystalline entomocidal protoxin) (130 kDa crystal protein)
 DE Name-cry9Aa; Synonyms-cryIG, cryIVA(a);
 GN Bacillus thuringiensis subsp. galleriae.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=29338;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 24-34.
 RC STRAIN=11-67;
 RX MEDLINE=92070568; PubMed=1660003; DOI=10.1016/0014-5793(91)81144-W;
 RA Smulevitch S.V., Osterman A.L., Shevelev A.B., Kaluger S.V.,
 RA Karsin A.I., Kadyrov R.M., Zagnitko O.P., Chestukhina G.G.,
 RA Stepanov V.M.;
 RT "Nucleotide sequence of a novel delta-endotoxin gene cryIG of Bacillus thuringiensis ssp. galleriae.";
 RL FEBS Lett. 293:25-28(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 1-1151.
 RC STRAIN=DSIR517;
 RX MEDLINE=92211129; PubMed=1556556;
 RA Gleave A.P., Hedges R.J., Broadwell A.H.;
 RT "Identification of an insecticidal crystal protein from Bacillus thuringiensis DSIR517 with significant sequence differences from previously described toxins.";
 RL J. Gen. Microbiol. 138:55-62(1992).
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut epithelial cells of insects. This protein is toxic to Galleria mellonella.
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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 CC -----

DR EMBL; X58120; CAA41122.1; -; Genomic DNA.
 DR EMBL; X58534; CAA41425.1; -; Genomic DNA.
 DR PIR; S19306; S19306.
 DR HSP; P02965; ICY.
 DR InterPro; IPR003305; Cenc carb bd.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin C.
 DR InterPro; IPR005639; endotoxin N.
 DR Pfam; PF02018; CBM_4_9; 1.
 DR Pfam; PF03944; Endotoxin C; 1.
 DR Pfam; PF00555; Endotoxin M; 1.
 DR Pfam; PF03945; Endotoxin N; 1.
 KW Direct protein sequencing; Sporulation; Toxin.
 FT PROPEP 24 23 Removed in mature form.
 FT CHAIN 24 1156 Pestidical crystal protein cry9Aa.
 SQ SEQUENCE 1156 AA; 129727 MW; 785F65B1B1165FF2 CRC64;
 Query Match 20.4%; Score 747; DB 1; Length 1156;
 Best Local Similarity 30.6%; Pred. No. 5.7e-43;
 Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;
 QY 9 NKNEYELLESSNNTNTPN--RYPPANNRDMSTWMDCCQ-----ISW-DEIWESVETITS 62
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 2 NQNKHGIIGASGCGCADDVAKYPLANNPYSSALNLSCONSSILNWINIIGDAAKEAVS 61
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 63 IGINLIEFVIEPSLGG-INTLLSIIGKLI-PTNQTVSALSTCDLLSIIRKEVADSVLSD 120
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 62 IGTIVSLITAPSLTGLISIVYDLIGLVGSSGOSTSDLSICDLSIIDRVSOVLSD 121
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 121 AIADFDGKLNKRYEYLYSLGAWLKDGKPLQKTNNSDYGQVYFKLSERDFNEIL---- 176
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 122 GIADFNGSVLYRN-YLEALDSWKN-----PNSASAEELTRPRIADSEFDRLTRGS 174
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 177 ---GSLSRNNAQVLLIPTFAQAAVOLLRLDRAVQYKAQW-----PFLSAENVRSBLI 228
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 175 LTNGGSLARQAQIILLPSFASAAFFHLLLRDATRYGTNNGLYNATPFINYQSKLVELI 234
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 229 SPNSGCDFTGDIYERLCKTAETNYCLYQVGLNQIKQGTGADTWSKFNKPERMTL 288
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 235 E-----LYTDYCVHWNRGNELRQGTATATALEFHYRREMTL 274
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 289 AVLDIILFIPTDYFEKYPPLTHVELTRIEYTDVAGY-----SSGTYSMWR--NWPNTFNGL 342
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 275 MVLIDIVASFSLDITNYPIETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNRR--FSDL 333
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 343 EANGTRGGLVTWLSKIGIYNEYVSRYPAG-----WVGRHYEDYTKGNGIFORMSGT 395
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 334 E-NAIPNPRPSWFLNNMIISTGSLTLPVSPSTDRARVWYSGRDRISPANSQFTELISGQ 392
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 396 TSNDLRNIDFONADYVYKITSIAIMNLVGETTARPEYRYSKADPRVGGFDLNDAGNGL 455
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 393 HTTATQTILGRN--IFRVDLSQA-CNL-NDTT-----YGNRAVF-----YHDASEGS 435
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 456 SRMTIESTFPLVLHNSGVGRP-----SHRLSNAACVVVG----- 489
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 436 QRSVYEG-----YIRTGIDNPRVQINITYLPGENSIDPTPEDYTHILSTINLTCGLRQV 491
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 490 ----NSRVNVYGVHTHTSLKRENIIEANQITQIPAVKSYLYQLANAYTYVIKGTHTCGD 545
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 492 ASNRSSLVMYGWTHTKSLARNNTINPDRIQTPLTK-----VDTRGTGVSYVNDPGFIGGA 547
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 546 LIRFLRTKSEYNAVYAGGIGIRLIINNKTAGOSYRIRFRYADKAFFSVYLYPGGWSNR 605
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 548 LLQ-----RTDHGSL-----GVLRVQFPLHLRQOYRIRVRYASTTIRLSV-----NGS 591
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 QY 606 FVSLEKSYSGNY-----DOLKYSDFKFAEITPPLP-SSNIQMDVEMQANSFOSDVNVVLDDK 661
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 592 FGTISQNLPSMTWLGEDRLRYGSFAIRENTSIRTASPDQIRLIEPSFIRQEVYV--DR 649
 QY 662 IEFILPSNTTILEYEGERDLEKTKNAVNDLFT 692
 Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
 Db 650 IEFIPVNPTR--EAKEDLEAAKKAVASLFT 677

```
CC terminus.
CC -|- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U88188; AAC61891.1; -; Genomic DNA.
CC HSP; Q61117; J316.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
CC NON TER 674
CC SEQUENCE 674 AA; 75959 MW; DA3904DAB891C978 CRC64;
CC
CC Query Match 22.7%; Score 831; DB 1; Length 674;
CC Best Local Similarity 31.9%; Pred. No. 3.8e-49;
CC Matches 236; Conservative 131; Mismatches 257; Indels 116; Gaps 31;
CC
CC QY 4 MSPYQNKNEYEILESSNNNTNPNYPFANN-----RDMTMSW-NDCOG--ISWDEIWE 55
CC Db 1 MNQYQNKNEYEILESSNNNNMNPYPFADDPNAVMMKNGYKDWVNECEGNSVSPSAAA 60
CC
CC QY 56 SVETITSGINLIEFVIEPISLGGINTLLSIIGKLIPTNQTYSALSIDLLSIRKEVAD 115
CC Db 61 ITSQIVSVLTKLAKAVASSLA--DSIKSLGLSKITENNVSQVSNVQVHQLINRIQIE 118
CC
CC QY 116 SVLSDAIADPDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIG--QLVYYPFKLSERDF 172
CC Db 119 TILDGESSLGLVAIYNRDYLGALEAW-----NNKNSINYQTNVAAEAKTVVEREF 170
CC
CC QY 173 NEILGSLSRNNAQVLLPTFAQAANVOLLRLDRVQYKAQWPFPLSAENVRSELSPNS 232
CC Db 171 FTKLKIYTSSTQITLLPTFAQAANLHLSMLRDVAMYQEGW-----NLQSHL----- 218
CC
CC QY 233 GCDFTGDYERLCKTAETNYCLYVQVGLNOIKQGGTADTWSKFNKFRREMTLAVLD 292
CC Db 219 -----NYSKELDDALEDYNYCEVYTKGLNALR--GSTAID-WLEFNSFRDMLTLMVLD 270
CC
CC QY 293 IIAIFPTYPEKPLPHVELTREIYTDVAGYSSGTSYSLRNWPNT-----FNGLEANG 346
CC Db 271 LVAIFFENYNVRYPLSTKISLSRKIVTDPVGRDTPS--FGDWTNTRGLANFNDLRELV 328
CC
CC QY 347 TRGPGLVTLWSKIGIYNEVSRV-----FAGVGTGRHYEDYT-KNGIIFORMSGTT- 396
CC Db 329 TDSPLSVKLGMDTIYTGAIYSRPTSPGDRIGWYGNINAFYHTGRTDVMVPRQTGDTA 388
CC
CC QY 397 ----SNDLRNIDFQNAADVYK--ITSIAIMNLVG--ETTARPEYRVSKADPRRVGGPDLY 448
CC Db 389 YEDPSTFISNLYD--DIYKLDRAAAVSTIQAMDIT---FGVSSSPFDIRGNQLY 442
CC
CC QY 449 DAGNGLSLRMTEISTEPLVLHNSG--VRGPSHRL-----SNAACVYVGNRSRVNVYGTW 500
CC Db 443 QS-NKPYPSLPITITPFGBESSSEGNANDYSHLLCDVKILQEDSSNICEGRSSILSHAWTH 501
CC
CC QY 501 TSKLRNIEIENAOITQIPAVKSYLQNYLANAYTVYIKGT-HTGGDLIRPLRTKSYNAV 559
CC Db 502 ASLDRNTILPDEITQIPAVTAYELR-----GNSSVAVGPGSTGGDLV-----KMSYHSV 551
CC
CC QY 560 YAGGGIRLIINNKTAGSYRIERYAADAAPF-----SVLYPCGGWSNRFVSLKSY 613
CC Db 552 WS----FKVYCSSEL---KNTRVRIRYASHGNCQFLMKRWSTGVAPQWARH---NVQGTFF 602
CC
CC QY 614 SGNYDDLKYSDFKFABIITPPLPSSNIQMDVENQANSFQSDVNVVLVDKIEFLPSNTTILE 673
CC Db 603 S---NSMRVEAPKYLDIFITTPENNFAFTIDLESG-----DLFDKIEFIPVSGSAFE 654
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QY 674 YGERDLEKTKQAVNDLFTN 693
Db 655 YEGKQNIETQRAVNDLFIN 674

RESULT 4
Q6BCH5 BACTU
ID Q6BCH5 BACTU PRELIMINARY; PRT; 675 AA.
AC Q6BCH5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Delta-endotoxin.
GN Name=cry24-like;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]_TaxID=1428;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96-OK-85-24;
RA Ohgushi A., Saitoh H., Wasano N., Ohba M.;
RT "Cloning and characterization of novel cry genes from a mosquitocidal
RT Bacillus thuringiensis serovar sotto strain";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB185105; BAD32657.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 675 AA; 75906 MW; E983D92F9053AEE8 CRC64;

Query Match 21.5%; Score 787; DB 2; Length 675;
Best Local Similarity 32.7%; Pred. No. 4.5e-46;
Matches 239; Conservative 109; Mismatches 286; Indels 96; Gaps 26;

QY 4 MSPYQNKNEYEILESSNNNTNPNYPFANN-----RDMTMSW-NDCOG--ISWDEIWE 55
Db 2 VNPYQNKKEVSFYEHSNNQKIDPNRYPTNPNNAVMMKNGYKDWVNECEGNSVSPSAAA 61
QY 56 SVETITSGINLIEFVIEPISLGGINTLLSIIGKLIPTNQTYSALSIDLLSIRKEVAD 115
Db 62 VTSALISIVLTKLAKALVSSL--VDAIKSSLSGISEVITKNNVSQLSMELVNQLINRIQIE 119
QY 116 SVLSDAIADPDGKLKNRYEYLSYLGAWLKDGKPLQKTNNSDIGQLVYYPFKLSERDFNEI 175
Db 120 TIMDLSGASLNGLMGIYKR--YLNALAEWDKD-----KSNITLQENVIEEFKYVESFPFN 173
QY 176 LGGSLSRNNAQVLLPTFAQAANVOLLRLDRVQYKAQWPFPLSAENVRSELISPSGCD 235
Db 174 LKGIYRTSSSQITLLPTFAQAANLHLSMLRDVAMYQEGW-----NLQSHL----- 218
QY 236 FTGDIYERLCKTAETNYCLYVQVGLNOIKQGGTADTWSKFNKFRREMTLAVLDITA 295
Db 219 ---DYKMELDIALKDYTYNCEVYVNRGLNALR--GSTAID-WLEFNSFRDMLTLMVLDVA 273
QY 296 IFFTDFEYKPLPHVELTREIYTDVAGYSSGTSYSLRNWPNT-----FNGLEANGTRG 349
Db 274 IFFNDYDVPQYPLPTKIGLSRKIYTPVGTTRTD--FGNWTLTDRLANFNDLREVDVDS 331
QY 350 PGLVTLWSKIGIYNEVSRV-----FAGVGTGRHYEDYTKNGIFQRMSTGTTNDL 400
Db 332 PSLVKWLVDMMNIYTGAIYSRPTSPGDRIGWYGNMNSFVLTSRSLSYNNYGEIAHED 391
QY 401 RNIDFQNAADVYKITSLA-----IMNLVGETTARPEYRVSKADPRRVGGPDLYDAGNGL 455
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QY 246 CKTAETNYCLWYOVGLNOIKOGGTGADTWSEKFKREMTLVLDTIITAIPTVDFPKY 305
DB 243 CKIAETDICEYWOAGLNOIKOAGTGADTWAKFNKFRMTLTVLDTIITAIPTVDFPKY 302
QY 306 PLPTHVELTREIYDAVGYSSGYSYSLRWNPNTFNGLEANGTRGPGLVTLWLSKIGIYNEY 365
DB 303 PLPTHVELTREIYDTPGVYSSGYSYSLRWKNTGAFNTLEANGTRGPGLVTLWLSIGIYNEY 362
QY 366 VSRYPAGWGTGTHYEDYTKNGIFQMSGTTNDLRNIDFQNAVYKITSLSIMNLVGET 425
DB 363 VSRYPAGWGTGTHYEDYTKNGIFQMSGTTNDLRNIDFQNAVYKITSLSIMNLVGET 422
QY 426 TARPEYRVSKADPRRVRGGPDLVADGNGLSKRWITESTPLVLHNSGRGP-----SH 478
DB 423 NARPEYRVSKADPRRVRGGPDLVADGNGLSKRWITESTPLVLHNSGRGP-----SH 476
QY 479 RLSNAACVYVGNRSNVVYGTWHTSLKRENIIEANOITQIPAVKSYVLYQVLANAYTVIK 538
DB 477 RLSNAACVAGNSRNVVYGTWHTSLKRENIIEANOITQIPAVKSYVLYQVLANAYTVIK 533
QY 539 GT-HTGGDLIRFLTKSEYNVAVAGGIRLIINNKTAGOSYRIRPRYAADKAAFFSVIY 597
DB 534 GPGHTGGNVVSL-----PYYSRLKIRLI--PASTNKNYLVRVYITSTS-----NGRLL 579
QY 598 PGWGSNRVFSLEKSY-----SGNVDDLKYSDFKFAEIIITPPLPSSNIQMDVEMQANSFQ 652
DB 580 VERNWSPS-----SIINSTFFLPSTPGDSFGYVD-----TLVTFNPGVEIILIONLD 627
QY 653 SDNVNVLDKIEFLPSNTTTLVEYGERDLKTKNAVNDLF 691
DB 628 TPIINV--DKVEIPVNSTALEYEGKQLEKADQVNDLF 664

RESULT 2
ID Q7X3F7 BACTA
AC Q7X3F7
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Putative mosquitoicidal toxin.
GN Name=crv40-like;
OS Bacillus thuringiensis (subsp. aizawai).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1433;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Bun1-14;
RA Ito T., Sahara K., Asano S., Bando H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB112346; BAC7648.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defence response; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR Pfam; PF03944; Endotoxin C; 1.
DR Pfam; PF00555; Endotoxin M; 1.
DR Pfam; PF03945; Endotoxin N; 1.
SQ SEQUENCE 666 AA; 75432 MW; F6B9E33309D06CDF CRC64;

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Query Match 47.7%; Score 1745; DB 2; Length 666;
Best Local Similarity 51.1%; Pred. No. 6.8e-113;
Matches 361; Conservative 107; Mismatches 181; Indels 58; Gaps 16;
QY 4 MSPYQNKNEYILESSNNNTNPNRYPFANRDMSTMSWNCQGISWBIWESVETITS 63
DB 1 MNSYQNKNEYILKSSPNNTNPNRYPFANRDMSTMSWNCQGISWBIWESVETITS 60

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QY 64 GINLIEFVIBSLGGINTLLSIIGKLIPTNRQTVSALSICOLLSTIRKEVADSVLSDA 123
DB 61 GIDLITFLGEPSTIGTINILFVIGKLLPSG-QNVASLSICOLLSTIRKEVADSVLSDAYG 119
QY 124 DFDGKLNRYEYLSYLGAWLKDGKPLQKTNNSDIGQVYVFKLSERDFNEITLGGSLRN 183
DB 120 DFGVNVNYQYVLTSLKWLDAKGP---TTGQLLTDTVKHFEFSERFENALLKGSLSRP 176
QY 184 NAQVLLPFAQAANVQLLLRLDAVQYKAQNPFPFLSAENVRSSELISPSNGCDFOTGYDER 243
DB 177 KGEILLPTTYQGANLHLLLRDFVQYKAVWEKELRTENVESELISPS--FDYEGHFKEQ 234
QY 244 LKCKTAETNYCLWYOVGLNOIKOGGTGADTWSEKFKREMTLVLDTIITAIPTVDFPKY 303
DB 235 L-----AEHINHCITWYQAGLNOIKESGTTSTENLWKNFKREMTLVLDTIITAIPTVDFPKY 290
QY 304 KYPLPTHVELTREIYDAVGYSSGYSYSLRWNPNTFNGLEANGTRGPGLVTLWLSKIGIY 363
DB 291 NYKSETHIELSREVYTDVPGYN-----GWEQNLNGFNTLEANGTRGPGLVTLWLSKIDIFT 346
QY 364 EYVSRV-----PAGWGTGTHYEDYTKNGIFQMSGTTNDLRNIDFQNAVYKITS 415
DB 347 DEVTEYSGWSPVAILRGWAGTRHYEIVTGSNTLQRISSGTTSDVSNIDFINSRIPIITS 406
QY 416 LAIMNLVCEETAR---PEYRVSKADPRRVRGGPDLVADGNGLSKRWITESTPLVLHNSG 472
DB 407 LARYALAGAAAGNPGSPRYRVSVEFSTGRYTFLYEYVNSPGISSMTTESKLPVGNATG 466
QY 473 VRGSPHRLSNAACVYVGNRSNVVYGTWHTSLKRENIIEANOITQIPAVKSYVLYQVLANA 532
DB 467 FTDYFNRLSNAACVQFGTSRVNVYGTWHTSHGEGNYVYPNKITQIPAVKAWEIR-----G 521
QY 533 YTYVIKGT-HTGGDLIRFLTKSEYNVAVAGGIRLIINNKTAGOSYRIRPRYAADKAAAF 591
DB 522 TSSVAVAGPGHTGGNLV-----KMSYHSVWS---IKFTCQL---KRYRVIRYASDGNCCQ 570
QY 592 FSVLYPGWGSNRPV-----SLEKSYSGNVDDLKYSDFKFAEIIITPPLPSSNIQMDVEM 646
DB 571 LAMRRWRGGPG---YVQEARHTVQRTFSGS---MTYDSFKYLDIFMTFAEDYTFDLTIDL 624
QY 647 QANSFQSDNVNVLDKIEFLPSNTTTLVEYGERDLKTKNAVNDLF 693
DB 625 ESGG-----ALYIDKIEFIPDDLTTLVEYERNLEKTKNAVNDLF 666

RESULT 3
ID C24AA BACTJ STANDARD; PRT; 674 AA.
AC O87905;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pesticidal crystal protein cry24Aa (Insecticidal delta-endotoxin
DE CryXXIVA(a)) (Crystalline entomocidal protoxin) (Crystal protein)
DE (Insecticidal protein Jcg72) (Fragment).
GN Name=cry24Aa; Synonyms=cryXXIVA(a);
OS Bacillus thuringiensis subsp. jegathesan.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=56955;
RN [1]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RA Kawalek M.D., Gill S.S.;
RL "Isolation and characterization of insecticidal genes from Bacillus
RL thuringiensis subsp. jegathesan."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 11:08:04 ; Search time 232 Seconds
(without alignments)
2107.462 Million cell updates/sec

Title: US-10-781-979-3
Perfect score: 3655
Sequence: 1 MKQMSFYQNKVEILESSS.....YEGERDEKTNVNDLFTN 693

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2329.5	63.7	666	2	Q8VW62_BACTA
2	1745	47.7	666	2	Q7X3F7_BACTA
3	831	22.7	674	1	C24AA_BACTJ
4	787	21.5	675	2	Q6BCH5_BACTU
5	747	20.4	1156	1	Q99031_BACTG
6	745	20.4	1169	1	CR9AA_BACUK
7	729	19.9	660	2	Q8RQU5_BACTA
8	728.5	19.9	1160	1	CR8CA_BACTP
9	728.5	19.9	1160	2	Q6R2R6_BACTU
10	709	19.4	1144	2	Q8KZL7_BACTG
11	707.5	19.4	719	1	CR1ID_BACTU
12	705.5	19.3	1228	1	CR1BA_BACTK
13	704.5	19.3	1228	2	Q93NM5_BACTU
14	702.5	19.2	1228	1	CR1BA_BACTE
15	702.5	19.2	1228	2	Q93T75_BACTE
16	690.5	18.9	675	1	C25AA_BACTJ
17	689	18.9	849	2	Q6PYW8_BACTK
18	689	18.9	1227	1	CR1BE_BACTU
19	680	18.6	1215	1	CR1KA_BACTM
20	680	18.6	1231	2	Q8KNY2_BACTU
21	679	18.6	719	1	CR1IA_BACTK
22	679	18.6	719	2	Q6X181_BACTU
23	679	18.6	719	2	Q546K2_BACTK
24	679	18.6	719	2	Q581W9_BACTU
25	679	18.6	720	2	Q4LDH4_BACTU
26	679	18.6	746	2	Q4W4S8_BACTU
27	678.5	18.6	719	1	CR1IB_BACTE
28	678	18.5	719	2	Q93NJ5_BACTU
29	678	18.5	1229	1	CR1BB_BACTU
30	678	18.5	1233	1	CR1BC_BACTM
31	677	18.5	1231	1	CR1BD_BACTZ

32	676	18.5	719	2	Q8KY61_BACTU	Q8ky61 bacillus th
33	674.5	18.5	719	2	Q9FOP8_BACTU	Q9fop8 bacillus th
34	673	18.4	719	2	Q85796_BACTK	Q85796 bacillus th
35	672	18.4	1157	1	CR8AA_BACUK	Q45704 bacillus th
36	659	18.0	686	2	Q75QO5_BACTE	Q75qo5 bacillus th
37	636.5	17.4	1163	2	Q5XLA8_BACTP	Q5xla8 bacillus th
38	636	17.4	659	1	CR3BA_BACTO	P17969 bacillus th
39	631.5	17.3	852	2	Q643Z7_BACTU	Q643z7 bacillus th
40	631.5	17.3	852	2	Q9S6N9_BACTU	Q9s6n9 bacillus th
41	627.5	17.2	652	2	Q6PXN8_BACTU	Q6pxn8 bacillus th
42	624.5	17.1	644	1	CR3AA_BACTD	P0a381 bacillus th
43	624.5	17.1	644	1	CR3AA_BACTM	P0a380 bacillus th
44	624.5	17.1	644	1	CR3AA_BACTT	P0a379 bacillus th
45	623.5	17.1	644	2	Q5EGP3_BACTT	Q5egp3 bacillus th

ALIGNMENTS

RESULT 1
Q8VW62_BACTA
ID Q8VW62_BACTA PRELIMINARY; PRT; 666 AA.
AC Q8VW62;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative mosquitoicidal toxin (fragment).
GN Name=crv40A;
OS Bacillus thuringiensis (subsp. aizawai).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1433;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ito T., Sahara K., Amano S., Bando H.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB074414; BAB72018.1; -, Genomic_DNA.
DR HSSP; Q06117; 1J16.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0030435; P:sporulation; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR000834; Peptidase_M14.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 666 AA; 75311 MW; A87853FAE8FAM41D CRC64;

Query Match	63.7%;	Score	2329.5;	DB 2;	Length	666;			
Best Local Similarity	67.2%;	Pred. No.	1.2e-153;						
Matches	470;	Conservative	62;	Mismatches	116;	Indels	51;	Gaps	12;
QY	7	YQNKVEYEI	LESSSSNTNTPNRYPFANRDMSTMWNSDCCQISWDEIWESVETITSIGIN	66					
Db	3	YENKVEYEI	LESSSSNTNPNRYPFANDRDMSTMWNSDCCQISWDEIWESAETITSIGID	62					
QY	67	LIEFVIEPSL	GGINTLLSIIGKLIPTNRQTVSALSICDILLSIRKEVADVSLSDAIDAF-	125					
Db	63	LIEFLMEPSL	GGINTLFSIIGKLIPTNHQVSALSICDILLSIRKEVADVSLSDAICRFL	122					
QY	126	DGKLKNRYEY	LSYLGAWLKDGKPKQKTNNSDIGLVYFKLSRDFNEIILGGSLSRNA	185					
Db	123	DGKLKNRYEY	LPYLGAWLKDGKPKQKTNNSDIGLVYFKLSRDFNEIILGGSLSRNA	182					
QY	186	QVLLLP	TFAQANVQLLRDAVQYKAQWFPFLSAENVRSSEIISPNSGCDFTGDIYERLK	245					
Db	183	QILLLP	YFCASCKCOLLRDAVQYEQWFPFLSAENVRSSEIISPNSGCDFTGDIYERLK	242					

C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C;Accession: I39811
R;Donovan, W.P.; Rupa, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burke, M.C.; Johnson, T.B
Appl. Environ. Microbiol. 58, 3921-3927, 1992
A;Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal crys
A;Reference number: I39811; MUID:93119147; PMID:1476436
A;Accession: I39811
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-652 <RES>
A;Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:g142729; PIDN:
C;Genetics:
A;Gene: cryIIIB2
C;Superfamily: Parasporal crystal protein

Query Match 16.6%; Score 605; DB 2; Length 652;
Best Local Similarity 27.6%; Pred. No. 4.7e-33;
Matches 201; Conservative 141; Mismatches 241; Indels 146; Gaps 35;

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QY 4 MSPVQNKNEYEILESSNN--TNTNRYPFANNRD--MSTMWNDCQGISWDEIWE---55
DB 1 MNP-NRSEHDTIKVTPNSELOTN-HNQYPLADNPNSTLEELNYKGFRLWTESDSSTEVL 58
QY 56 --SVETITSGINLIEFVI---EPLSGGINTLL-SIIGKLIPTNRQTVSALSICDLLSI 108
DB 59 NSIVKDAVGTGISVVGQILGVGVPPAGALTSFYQSFINTIMFSDADPWKAP-MAQVEVL 117
QY 109 IRKEVADSVLSDAIADPGKLNRYREYLSYLGAWLKDGKPLQKTNNSDIGQLVYFVKLS 168
DB 118 IDKIEEYAKSKALAELOQ-LQNNFEDYNALNSWKTKPLSLRSKRSQD--RIRLEFSQA 174
QY 169 ERDFNEILGSLSRNNAQVLLLPFAQAANVQLLLRDVAVQYKAQWFPFLSAENVSELI 228
DB 175 ESHFRNSM-PSFAVSKPEVLFLPTYAQAANTHLLLDKDAQVGESEW--GYSSSDV----226
QY 229 SPNSGCDFTGDYERLCKCTAEYNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTL 288
DB 227 -----AEFVHRQLKLTQYTDHCVWYVGLNGLR--GSTYDAWVKNFRREMTL 275
QY 289 AVLDDIIAIPPTYDFEKYPLPHTVELTREIYTDVAGYSSGTYSWLRNMPNFTNGLEANTR 348
DB 276 TVLDDLIVLFPFYDIRLYSKGKVELTRDIFTDPI-FSLNT---LQEGYPTFLSIE-NSIR 330
QY 349 GPGLVTLWLSKIGIYNEVSVRYFAGWGTGRHYEDYTKNGIFQFMS-----GTT 396
DB 331 KPHLFYLOGI-----EFHTRLQPGYFGKOSF-NYWSGNYVETRPSTGSSKTIITSPYGDK 385
QY 397 SND-LRNIDPQNAADVYKITSALIMNLVGETTARPEYRVSKADPRRVGGPDNLNDAGNGL 455
DB 386 STEPVQKLSFDGQKYR--TIANTDVANWPNKGKYLGVTKVDSQ-----YDDQKNET 436
QY 456 SRMTIESTPPLVLHNSG-----VRGPHRLSNAACVVYGNR--V 493
DB 437 STQYDSK-----RNNGHVSAQSDIDQLPETTDEPLEKAYSHOLNYAECFLMQDRRTI 491
QY 494 NVYGTWHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVYIKT-HTGGDLIRFLRT 552
DB 492 PFTWTHRSVDFNTIDAELITPLPVKAYALSSGAS-----IIEGPGFTGGNLL-FLKE 545
QY 553 KSEYNVAYAGGGRLLIINNKTAGQSVYRIRPRYAA-----DKAAPFVSVLYPGWG 602
DB 546 SSNSIAKF-----KVTLNSALLQRYRVRIRYASTNLRFLVQNSNDFLVIYI-----594
QY 603 SNRFVLSKSYSGNYDDLYSDPKFAEIIITPPLPSSNI-----QMDVEMQANSFQSDVNV 657
DB 595 -NKTMKD-----DDLTYQTDLA-----TTNSNMGFSGDKNELIIGAESFVSNEXI 640
QY 658 VLDKIEFLP 666
DB 641 YIDKIEFIP 649
```

RESULT 15

S39536

Parasporal crystal protein cry9Ba1 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
C;Species: Bacillus thuringiensis
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 05-Oct-2004
C;Accession: S39536
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepan
FEBS Lett. 336, 79-82, 1993
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bac
A;Reference number: S39536; MUID:94085596; PMID:8262221
A;Accession: S39536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <SHE>
A;Cross-references: UNIPROT:Q45745; UNIPARC:UPI00001781A3; EMBL:X75019
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 16.5%; Score 603.5; DB 2; Length 1154;
Best Local Similarity 28.4%; Pred. No. 1.3e-32;
Matches 200; Conservative 107; Mismatches 253; Indels 143; Gaps 30;

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QY 56 SVETITSGINLIEFVIEP---SLGGINT--LLSIIGKLIPTNRQTVSALSICDLLSIIR 110
DB 50 NVRTGLQTGIDIVAVVVGALGCPVGILTGFLSTLFGFLWPSNDQAWFAFIQMEELIE 109
QY 111 KEVADSVLSDAIADPGKLNRYREYLSYLGAWLKDGKPLQKTNNSDIGQLVYFVKLSER 170
DB 110 QRISDQVVRTALDGLTG-IQYNYQYLIALKEW-----EERPNGVRANLVLRQFELIHA 162
QY 171 DFNEIL---GGSLSRNNAQVLLLPFAQAANVQLLLRDVAVQYKAQWFPFLSAENVSELI 227
DB 163 LFWSSMPSPGSGGSGRFOAQLLVYAQAANLHLLLDADAKEYGARW-----GURESQ 215
QY 228 IPSNSGCDFTGDYERLCKCTAEYNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMT 287
DB 216 IG-----NLYFNELOTRTRDYTNHCYNVYNGLAGLR--GTSAESLWKYHQFREAT 265
QY 288 LAVLDIIAIPPTYDFEKYPLPHTVELTREIYTDVAGYSSGTYS-----WLRNMPNT 338
DB 266 LMADLIALFPYNTNRRYPIAVNPQLTREYVTDPLGVPSSESLFPELCLRWQETSAMT 325
QY 339 ENGLEANGTRGGLVTLWSKIGIYN-----EYVSRYFAGWGTGRHYEDYTKG-----NG 387
DB 326 FSNLENAIISPHLFDFTINNLMITYGSPSVHUTNQLIEGWIG---HSVTSSLLASGPTT 381
QY 388 IFQMSGTTSNDLRNIDFONADVYKI-----TSLAIMNLVGETTARPEYRVSKADPRRVG 442
DB 382 VLRRNYGSTISVNYFSEFNDRDVYQINTRESHTGLGFQN-----APLFGITPAQF----430
QY 443 GPDNLVDAGNGLSR---WTIESTPPLV-----LHNSG---VRGPHRLSNAACVVY----488
DB 431 -----YPGGYTSVTQORNALTCQNTYSIDELPSLPNEPISRSYSHRLSHITSYLHRVLT 485
QY 489 -----CNSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYLQNYLANAYTVYIKGT 540
DB 486 IDGINYSGN--LPTYVWTHRDVDTLTNTIADRITQLPLVKSFEIP-----AGTTVVVRGP 538
QY 541 -HTGGDLIRFLRTKSEYNVAYAGGGRLLIINNKTAGQSVYRIRPRYAAADKAAPFVSVYL---596
DB 539 GFTGGDILR--RT-----GVGTFFGTVIR-VRTTAPLTQRYRIRFRFASTTNLFIGIRVGDR 590
QY 597 -----YPGWGSNRFVLSKSYSGNYDDLYSDPKFAEIIITPPLPSSNIQMDVEM-----QAN 649
DB 591 QVNYFDFGRTMNR-----GDELRYESFATREFTT----DFNFRQPQELISLVFAN 635
QY 650 SFQSDVNVVLDKIEFLPSTNTTILEYGERDLEKTKYNAVNDLET 692
DB 636 AFSAGQEVYFDRIEIIIPVNPAP---EAKEDLEAAKKAVALSLFT 675
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Search completed: December 15, 2005, 11:19:58
Job time : 45 secs

A:Title: Functional analysis of block 5, one of the highly conserved amino acid sequence
A:Reference number: S48691; MUID:94307434; PMID:7913448
A:Accession: S48691
A:Molecule type: DNA
A:Residues: 667-676 <NIS>
A:Cross-references: UNIPARC:UPI0000017819A
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

```
Query Match      16.6%; Score 606.5; DB 2; Length 1180;
Best Local Similarity 28.7%; Pred. No. 8.7e-33;
Matches 223; Conservative 117; Mismatches 277; Indels 159; Gaps 42;

QY  4 MSPYQNKNEYETLSSNNNTNPN---RYPPANN-----RDMSTWSW-NDQC-----GIS 49
DB  1 MNPYQNKNEYETLNASOKKLINSNRYPIENSPKQLQSTNYKDWMLNMCQOQYGGD 60
QY  50 WDEIWESVE---TITSIGINLIEFVIEPSLG---GINTLLSIIGKLIPTNRQTVS-AL 100
DB  61 PETFIDSGELSAVTIV-VGTVLTGFGFTPLGLALIGFTLIPV---LPPAQDQSNWSD 116
QY  101 SICDLLSIIRKEVASVLSDAIDPDGKLNRYEY-----YLSYLGAWLKDGKPKLOKTN 155
DB  117 FITQTKNIIKKEIASTYSNA-----NKILN-RSFNVISTYHNHLKTWENNPNP---QNT 167
QY  156 SDIG---OLVYFVKLSERDFNEI---LGGSLSRNNA-----QVLLPTPFAQANVQLLLL 204
DB  168 QDVRTQIQLVHY-----HFQNVIPELVNSCPNPSDCDYNNILVSSYAQAANLHLTVL 221
QY  205 RDAVOYKAQWPFPLSAENVRSSELISPNSCGDTGDIYERLCKTAETNYCLYVYQVGLN 264
DB  222 NQAVKFEA---YLK-NNRQFDYLEP---LPTAIDYYPVLTKAIEDYNYCVTYTKKGLN 273
QY  265 QIK-----QCGTGADTWKFNKFRREMTLAVLDIIAIFPTDYDEKYPPLTHVELTREIYTD 320
DB  274 LIKTPDSNLGDNINWNTYRTKMTTAVLDVALFPNDYDVGKYPGVQSELTRIEY-Q 332
QY  321 AVGSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIGIYNE---YVSRYFAGWVGR 377
DB  333 VLNFEESPKYY-----DFQYQEDSLTRRPHLFTWLDLSLNFYEKAQTTPNNPF-----TS 382
QY  378 HYE---DYTKGNGIIFORMSGTTSNDLRNIDFQNAVYKITSLA-----IMNLVG-ETTAR 428
DB  383 HYNMFHYTLDN-ISQSSVFGNHNV-----TDKLSLGLATNIYIFLLNVLSDNKYL 434
QY  429 PEY-RVSKADF-----RRVGGPDLYDAGNN--GLSRMTIESTPPLVLSHNGV 473
DB  435 NDYNNISKMDFFITNGTRLLEKELTAGSGQITYDVNKNIFGL-----PILKRRENQ 485
QY  474 RGP-----SHRLS---NAACVYVGNRVNVTGHTSLKRENIIEANQITQIPAVK 521
DB  486 GNPTLFPPTYDNYSHILSPFKLSIPATYKTQVYTFANWTHSSVDPKNTIYTHLTQIPAVK 545
QY  522 SYLLQNYLANAVTYVYKGTHTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIR 581
DB  546 A-----NSLGTASKVQVGGCHTGGDLIDF---KDHF-----KITQHSNFOQSYFIR 589
QY  582 FRYAADKAAPFSVYL---YPGGWSGNRFVSLSEKSYSG-NYDDLKYSDPKFABIITPPLPS 637
DB  590 IRYASNGSANTRAVINLSIPG--VAELGMLNLPFTSGTDYTNLKYDKQFYLESNEVKFA 647
QY  638 SNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTILEYEGERDLEKTKNANDLFTN 693
DB  648 PNQNISLVNRSDDVYNTNTVLIDKIEFLPITRSIREDEKQKLETVQQLINTFYAN 703
```

RESULT 13

I39870

parasporal crystal protein ISRH4 - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C:Accession: I39870
R:Sen, K.; Honda, G.; Koyama, N.; Nishida, M.; Neki, A.; Sakai, H.; Himeno, M.; Komano,

Agric. Biol. Chem. 52, 873-878, 1988
A:Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes
A:Reference number: I39869
A:Accession: I39870
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-1180 <RES>
A:Cross-references: UNIPROT:P16480; UNIPARC:UPI0000001BLF; GB:D00248; NID:G216289; PIDN
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

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Query Match      16.6%; Score 605.5; DB 2; Length 1180;
Best Local Similarity 28.7%; Pred. No. 1e-32;
Matches 223; Conservative 117; Mismatches 277; Indels 159; Gaps 42;

QY  4 MSPYQNKNEYEILSSSSNNNTNPN---RYPPANN-----RDMSTWSW-NDQC-----GIS 49
DB  1 MNPYQNKNEYETLNASOKKLINSNRYPIENSPKQLQSTNYKDWMLNMCQOQYGGD 60
QY  50 WDEIWESVE---TITSIGINLIEFVIEPSLG---GINTLLSIIGKLIPTNRQTVS-AL 100
DB  61 PETFIDSGELSAVTIV-VGTVLTGFGFTPLGLALIGFTLIPV---LPPAQDQSNWSD 116
QY  101 SICDLLSIIRKEVASVLSDAIDPDGKLNRYEY-----YLSYLGAWLKDGKPKLOKTN 155
DB  117 FITQTKNIIKKEIASTYSNA-----NKILN-RSFNVISTYHNHLKTWENNPNP---QNT 167
QY  156 SDIG---OLVYFVKLSERDFNEI---LGGSLSRNNA-----QVLLPTPFAQANVQLLLL 204
DB  168 QDVRTQIQLVHY-----HFQNVIPELVNSCPNPSDCDYNNILVSSYAQAANLHLTVL 221
QY  205 RDAVOYKAQWPFPLSAENVRSSELISPNSCGDTGDIYERLCKTAETNYCLYVYQVGLN 264
DB  222 NQAVKFEA---YLK-NNRQFDYLEP---LPTAIDYYPVLTKAIEDYNYCVTYTKKGLN 273
QY  265 QIK-----QCGTGADTWKFNKFRREMTLAVLDIIAIFPTDYDEKYPPLTHVELTREIYTD 320
DB  274 LIKTPDSNLGDNINWNTYRTKMTTAVLDVALFPNDYDVGKYPGVQSELTRIEY-Q 332
QY  321 AVGSSGTYSWLRNWPNTFNGLEANGTRGPGVLTWLSKIGIYNE---YVSRYFAGWVGR 377
DB  333 VLNFEESPKYY-----DFQYQEDSLTRRPHLFTWLDLSLNFYEKAQTTPNNPF-----TS 382
QY  378 HYE---DYTKGNGIIFORMSGTTSNDLRNIDFQNAVYKITSLA-----IMNLVG-ETTAR 428
DB  383 HYNMFHYTLDN-ISQSSVFGNHNV-----TDKLSLGLATNIYIFLLNVLSDNKYL 434
QY  429 PEY-RVSKADF-----RRVGGPDLYDAGNN--GLSRMTIESTPPLVLSHNGV 473
DB  435 NDYNNISKMDFFITNGTRLLEKELTAGSGQITYDVNKNIFGL-----PILKRRENQ 485
QY  474 RGP-----SHRLS---NAACVYVGNRVNVTGHTSLKRENIIEANQITQIPAVK 521
DB  486 GNPTLFPPTYDNYSHILSPFKLSIPATYKTQVYTFANWTHSSVDPKNTIYTHLTQIPAVK 545
QY  522 SYLLQNYLANAVTYVYKGTHTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOSYRIR 581
DB  546 A-----NSLGTASKVQVGGCHTGGDLIDF---KDHF-----KITQHSNFOQSYFIR 589
QY  582 FRYAADKAAPFSVYL---YPGGWSGNRFVSLSEKSYSG-NYDDLKYSDPKFABIITPPLPS 637
DB  590 IRYASNGSANTRAVINLSIPG--VAELGMLNLPFTSGTDYTNLKYDKQFYLESNEVKFA 647
QY  638 SNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTILEYEGERDLEKTKNANDLFTN 693
DB  648 PNQNISLVNRSDDVYNTNTVLIDKIEFLPITRSIREDEKQKLETVQQLINTFYAN 703
```

RESULT 14

I39811

parasporal crystal protein cry3Bb1 - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cryIIIB2
C:Species: Bacillus thuringiensis

A;Gene: cryIIIA
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 17.3%; Score 631.5; DB 2; Length 652;
-Best Local Similarity 28.0%; Pred. No. 7.6e-35;
Matches 200; Conservative 143; Mismatches 255; Indels 117; Gaps 32;

QY 2 KKSPYQNKEYEILESSNNTTPN--RYPPAN--NRDMSWNCDCIGISWDIEVESV 57
|||:|||:::||||:
DB 7 RKNP-NRSEHDTIKTENNEVPTHVQPLAETPNTLEDLNKFLRWADNTEAL 65
|||:|||:::||||:
QY 58 ETITSGINLIEFVIEPSLGINTLLSIIIGKLIPTRQTVSALS----- 101
|||:|||:::||||:
DB 66 DSSTT-----KDVIQKGISVWGDLGVG--PFPGCALVSFYTNELTIWPSDPMKAF 117
|||:|||:::||||:
QY 102 ICDLLSIIRKEVADVLSDAIAPDFGLKNRYREYL SYLAWLKDGKPLKOTNNSDTGOL 161
: : : : |||:::||||:
DB 118 MEQVEALMDOKIADIYAKNKALAELOG--LQNNVEDYVSALSWSQKN--PVSRPNHSQGRI: 171
|||:|||:::||||:
QY 162 VIYFKLSERDFNEILGGSLRNNAOVLILLPTFAQAANNQLLLRLDVAQVKAOWPFPLSAE 221
|||:|||:::||||:
DB 175 RELFSQABSHFRSM--PSFAISGEVLFLLTYAQAAANTHLFLKDAQIQEGEE----- 226
|||:|||:::||||:
QY 222 NVRSSELISPNSGCDFTDYYERLKCKTAETNTCLYVQVQGLNQIKOGGTGADTWKSFNK 281
|||:|||:::||||:
DB 227 GYEKEDIA-----EFYKRQKLKTQEYTDHCWKVNVGDKLR--GSSYESWNFN 275
|||:|||:::||||:
QY 282 FREMTLAVLDIIAIPTDYDEKYPIPTHVELTREIYTD-AVGYSSTGYSWLKNWPFTN 340
: : : : |||:::||||:
DB 276 YRREMTLTVLDLIAFLPYDVRLYPKEVKTELTRDLVTDPIVGNV-----LRGYGTFS 330
|||:|||:::||||:
QY 341 GLBANGTRGPLVTWLSKIGIYNEYVSVRPAGVGRHYEDYTKNGCIFORMS----- 393
|||:|||:::||||:
DB 331 NIB-VYRKPHLFDYLHRI----QFTRFPQGYGNDSP--NYWNGNVSTRPSIGSDII 384
|||:|||:::||||:
QY 394 -----GTTSENDRINDIFQNADYKI---TSLAIMNLVGETTARPEYRVSKADFRRVG-- 442
|||:|||:::||||:
DB 385 TSPFYGNKSSEPQNLEFGCEKVYRAVANLAVM-----PSAVYSGVTKEVFSQYNDQ 438
|||:|||:::||||:
QY 443 ---GPDLNYDAGNN--GLSRMTIESTFPLVLHNSGVRGPSHRLSNAACVYVGNR--VN 495
|||:|||:::||||:
DB 439 TDEASTQTYDSKENVGAVSWSIDQLPETTDPLEKGYSHQLNVYMCFLMQSGRGTPV 498
|||:|||:::||||:
QY 496 YGWHTSLKRENILEANOITQIPAVSYLYONLANAYTVVIKGTH--TGGDLIRFLRTKS 554
|||:|||:::||||:
DB 499 LTWTHKSVDPFNMI DSKKITQLPLVAKYLKOSAS-----VWAGPRFTGDGIIOCTENG 553
|||:|||:::||||:
QY 555 EYNNAVAGGGIRLIINNKTAGSQYRIFRYAADKAFFSVLYLPGGMGSNRFVLSLEKSYS 614
|||:|||:::||||:
DB 554 A-ATLY-----VTPDVSYSQYARIHVASTISQITFTLSL--DGAPPFQQYV-FDKTIN 602
|||:|||:::||||:
QY 615 GNYVDLIKYSDFKABIITP--PLPSSNIQMDVEMOANSFQSDVNVLVDKIEFLPSN 668
|||:|||:::||||:
DB 603 KG-DLTLYSNSFNLASFTPPELGGNNLIQGV---TGLSAGDKVYIDKIEFIPVN 652
|||:|||:::||||:

RESULT 10
B29838
parasporal crystal protein - Bacillus thuringiensis subsp. israelensis (fragmen
C;Species: Bacillus thuringiensis subsp. israelensis
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C;Accession: B29838
R;Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfr
J. Bacteriol. 166, 801-811, 1986
A;Title: Structural similarity between the Lepidoptera- and Diptera-specific in
A;Reference number: A94672; MUID:86223796; PMID:3011746
A;Accession: B29838
A;Molecule type: DNA
A;Residues: 1-934 <RHO>
A;Cross-references: UNIPROT:P09662; UNIPARC:UPI00001781A0; GB:M12662; NID:g1432

Query Match 16.9%; Score 617.5; DB 2; Length 934;

C;Genetics:
A;Gene: cry3V
C;Superfamily: Paraaporal crystal protein
C;Keywords: Delta-endotoxin

Query Match 18.5%; Score 676; DB 2; Length 719;
Best Local Similarity 31.0%; Pred. No. 8.6e-38;
Matches 226; Conservative 118; Mismatches 284; Indels 122; Gaps 33;

Qy 3 KMSPYQNKNEYEILESSNNNTNTPNRYPPANNRDMSTMWDCOGISWDIWE---SVET 59
Db 20 KISTDSLKNETDI-----ELQINIHEDCLKSEYENVEPFVSAST 59
Qy 60 I-TSIGT--NLIEFVIEPSLGGINTLLS-IIGKLIPTNRQTVSALSICDLLSIIRKEVAD 115
Db 60 IQTGIGIAGKILGTGLVFPFAGQVASYLSFILGLMPKKGKQWE-IFMEHVEEIIINKIST 118
Qy 116 SVLSDAIADFDGKLNRYEYLSVLGAWLKDGPLOKTNNSDIGQLV--YFVKLSERDEN 173
Db 119 YARKALTDLKG-LGDALAVYHDSLESWGN-----RNNTRARSVVKSQYIAL-ELMFV 170
Qy 174 EILGGSLSRNAQVLLLPPTFAQAANVQLLLRDVAVQYKAQWFPFLSAENVRSBELISPSNG 233
Db 171 QKL-PSFAVSGEEVPLLPPIVAQAANLHLLLRDASIFGKEW--GLSSSEIST-----219
Qy 234 CDTGDIYERLCKTAEYNYCLYVYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDI 293
Db 220 -----FYNQVERAGDYSYHCKWYSTGLNNLR--GTNAESWRYNQFRDRMTLAVLDL 271
Qy 294 IAIPTTYDFEKYPLPTHVELTREIYTDVAVG-----YSSGTYSWLRNWPNTFNGLEANG 346
Db 272 VALFPSYDTQYPIKTTAQUTREYVTDATGVHPHPSFTSTT--WYNNNAPSFAIEAAV 329
Qy 347 TRGPGVLVLSKIGIYNEYVSR-----YFAGWVGRHYEDYTKGNGIFQMSGTTSDNLR 401
Db 330 VRNPHLLDFLEQVTVYS-LLSRNSNTQYNNMW-GGHKLEPRTTIGTLINTSTQGSTWTSIN 387
Qy 402 --NIDFQNAVYKITSIAIMNLVGETTARPEYRVSKADF--RRVGGP---DLNYDAGNNG 454
Db 388 PVTLPFTSRDVRVYTESLAGLNLF---LTQPVNGVPRVDHFHKVTHPIASDNFYPYGYAG 444
Qy 455 LSRMTTIESFTPLVLHSGN---VRGPGSHRLSNAACVYVGNRVNNGYVWTHTSLKRENIIEA 511
Db 445 IGTQLQDSENELPEATGQBNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTTIEP 504
Qy 512 NQITQIPAVKSYLYQNYLANAYTVVIKGT-HTCGDLIRFLRTKSEYNAVYVAGGIRLIIN 570
Db 505 NSITQIPLVKAFNLSSGA-----VVRGPGFTGCDILRNTTGT-----FGDIRVNIIN 552
Qy 571 NKTAGQSYRIRFYAADKAAFFSVYLYPGGWGNRFRVLSKYSYGNV-----DDLKYS 623
Db 553 PPPA-QRYRVIRIYASTDLQFHTSI--NGKALNQ-----GNFSATMNRGEDLDYK 600
Qy 624 DKFAEIIITPPLPSSNIQMDVENQANSFQSDVNVVLDKIEFLPSNTTILEYGERDLEKT 683
Db 601 TFRVTG-FTTPFSLDVQSTFTTIGAWNFSSGNEVDRIEFVPEVET---YEAYDFEKA 656
Qy 684 KNAVNDLFTN 693
Db 657 QEKVTAFTIS 666

RESULT 8
S10228
paraaporal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)
N;Alternate names: coleopteran-active paraaporal crystal protein; delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: S10228
R;Sick, A.; Gaertner, F.; Wong, A.
Nucleic Acids Res. 18, 1305, 1990
A;Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Ba
A;Reference number: S10228; MUID:90206811; PMID:2320431

A;Accession: S10228
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-659 <SIC>
A;Cross-references: UNIPROT:P17969; UNIPARC:UPI0000126C13; EMBL:X17123; NID:g40258; PID

C;Genetics:
A;Gene: cry3IIB
C;Superfamily: Paraaporal crystal protein
C;Keywords: Delta-endotoxin; toxin

Query Match 17.4%; Score 636; DB 2; Length 659;
Best Local Similarity 28.6%; Pred. No. 3.9e-35;
Matches 207; Conservative 141; Mismatches 243; Indels 134; Gaps 34;

Qy 2 KMSPYQNKNEYEILESSNN---TNTPNRYPPANNRD---MSTMWDCOGISWDEIWE 56
Db 7 RKMNP-NRSEYDTIKVTNPSELPTN-HNQYPLADNPNSLLEELNYKEFLRMTADNSTEV 64
Qy 57 VETIT-----SIGINLIEFVI-----EPSLGGINTLL-SIIGKLIPTNRQTVSALSICDLL 106
Db 65 LBSSTYKDAVGTGISVVGQILGVGVFPFAGALTSFYQSFLNAIWPSPDADPWKAF-MAQVE 123
Qy 107 SIIRKEVADSVLSDAIADFDGKLNRYEYLSVLGAWLKDGPLOKTNNSDIGQLVYFVK 166
Db 124 VLIDKKIEYAKSKALAELOG-LQNNFEDYVNALDSWKKAPVNLRRSQD--KIRELFS 180
Qy 167 LSERDFNEILGGSLSRNAQVLLLPPTFAQAANVQLLLRDVAVQYKAQWFPFLSAENVRS 226
Db 181 QAESHFRNSM-PSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGSEW--GYSSEDI---234
Qy 227 LISPNSGCDFTGDYERLCKTAEYNYCLYVYQVGLNQIKQGGTGADTWSKFNKFRREM 286
Db 235 -----AEFYQRLKLTQYTDHCVNWNVGLNSLR--GSTYDAWVKFNFRREM 281
Qy 287 TLAVLDLIAIFPTQPEKYPLPTHVELTREIYTDVAVGSSGTYSWLRNWPNTFNGLEANG 346
Db 282 TLTVLDLILVLPFPYDRLYSKGVKTELTRDITFDPI-----FTLNALOEYGTFTSSIE-NS 336
Qy 347 TRGPGVLVLSKIGIYNEYVSRVYFAGWVGRHYEDYTKGNGIFQMSGTTSDN-----399
Db 337 IRKPHLPDYLRGI-----EFHTRLRPGYSGKDSF-NYWSGNYVETRPS-IGSNDTITSPPY 390
Qy 400 -----LRNIDFQNAVYKITSIAIMNLVGETTARPEYRVSKADPRRVGGPDLNDYAGN 452
Db 391 GDKSIEPIQKLSFDGQKQYR--TIANTDIAAPDGKIYFGVTKVDFSQ-----YDDQK 441
Qy 453 NGLSRMTTIESFTPLVLHSGNVRGP-----SHRLSNAACVYVGNR 492
Db 442 NETSTQTYDSK-----RYNGYILGAQDSIDQLPPTTDEPLEKAYSHQLNTAECLMQDRR 496
Qy 493 --VNVYGWTHTSLKRENIIEANQITQIPAVKSYLYQNYLANAYTVVIKGT-HTGGDLIRF 549
Db 497 GTIPFTWTHRSVDFTNTIDAEEKITQLPVVKAYALSSGAS-----IIEGPGFTGGNLL-F 550
Qy 550 LRTKSEYNAYAGGIRLIINNKTAGQSYRIRFRVAADKAAFFSVYLYPGWGNRFPVSL 609
Db 551 LKSESSNAKFI-----KVTLSAALLQRYRVIRIYASTT---NLRLFQVN-SNNDPLVI 600
Qy 610 EKSYSQNYD-DLKYSDFKFAEIIITPPLPSSNIQW-----DVEMQANSFQSDVNVVLDK 661
Db 601 YINKTMNIDGDLTYQTDFDA-----TSNSNMFGSGDNTDPIIGAESFVSNKEIYIDK 652
Qy 662 IEFLP 666
Db 653 IEFIP 657

RESULT 9
A27323
paraaporal crystal protein cry3ha1 - Bacillus thuringiensis
N;Alternate names: coleopteran-specific insect control protein; crystal protein cryC; d
C;Species: Bacillus thuringiensis
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Oct-2004

QY 1 MKKMSYQNKV-----EYELLESSNNNTNTPRYFPANNRDMSTWSDCQGISWDEIWE 55
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1 MKLKNPDKQSSUNAKVKIATDSUKNETDIELKMNNEEDYLRMSSEH-----SIDPFVS 56
56 SVETIISIGI--NLIEFVIEPSLGGINTLLS--IIGKLIPTNRQTVSALSICDILLSIRKE 112
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 57 ASTIQIGIAGKILGTGVFPAGQIASLYSFLGELWPKGKQWE--IFMEHVEEIIQKIST 115
113 VADSVLSDAIADPDGKLNRYREYLYSLGAWLKDGKPLQKTNNSDIOQLV--YFVKLSR 170
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 116 ILTYARNKALSULRG--LGDALAVYHESLESW-----VENNRNTRARSVVKQYIAL--EL 167
171 DFNELIIGGSLSRNAOVLLLPFAQAAVQLLLRDVAVQYKAQWPFPLSAENVSELISP 230
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 168 MFVKQL--PSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW--GLSSASEIST----- 219
231 NSGCDFTGDIYERLCKTAETNYCLYQVGLNQIKQGGTGADTWKSKFRRREMTLAV 290
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 220 -----FYNQOVERAGDYSYHCVKYSTGLNLR--GTWAKSWVRNQPKDMLNV 268
291 LQIILFPYDEKYPPLPHVELTREIYTDVG-----YSSGTYSWLRNWPNTFNGLE 343
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 269 LDLVALFPSYDYLTVPIKTTSQLTREYVTDAGTVHPNQAFASFT--WYNNNAPSFSATE 326
344 ANGRCPGLVWLSKIGIYNEVSR-----YFAGWVGTRHYEDYTKNGIFORMSGTTSN 398
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 327 AAVIRSPHLLDFLEKVTIYS--LLSRWSNTQYNNMGHGR--LESRRPIGGALNTSTQGSTNT 384
399 DLK--NIDFQNAVYKITSLAIMNLVGETTARPEYRSKADF-----RVGGPDNLNYDAG 451
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 385 SINPVLQTSRDVRYTESLAGLNF--LTPVNGVPRVDFHMKFVTHPIASDNFYIYG 441
452 NGLSRMTIESTFPLVLHSG--VRGPHRLSNAACVYVGNRSRVNVTGHTSLKRENI 508
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 442 YAGVGTLQDSENELPPTTGPQNYESYSHRLSHIGLISASHVKALVSWTHRSADRTWT 501
509 IEANQITQIPAKSVYLYQNYLANAYTVIKGT--HTGGDLIRFLRTKSEYNVAVAGGIRL 567
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 502 IEFNSITQIPLKAFNLSSGAA-----VVRGPGFTGGDLIRRTNTGT-----FGDIRV 549
568 IINNKTAGQSYRIRFRYAADKAFFSVLYPGGWSNRFRVLSKYSYGN-----DDL 620
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 550 NINPPA--QRYVRIRYASTTDLQFHTSI--NGKAIQ-----GNFSATWNRGDL 597
621 KYSDFKFABIITPPLPSSNIQMDVEMQANSFQSDVNVLDKIEFLPSTNTTLEYEGERDL 680
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 598 DYKTFRTIG--FTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVT---YEAEDF 653
681 ETKNAVNDLFTN 693
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 654 ERAQEKVTAFTS 666

RESULT 6

I39814
insecticidal protein cryVI - *Bacillus thuringiensis*
C:Species: *Bacillus thuringiensis*
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C:Accession: I39814
R:Shin, B.S.; Choi, S.H.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A>Title: Distribution of cryV-type insecticidal protein genes in *Bacillus thuringiensis* tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I39814
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPARC:UPI0000036009; GB:L36338; NID:G540281; PIDN:AAC36999.1; PID:
C:Genetics:
A:Gene: cryVI
C:Superfamily: Parasporal crystal protein

Query Match 18.5%; Score 676; DB 2; Length 719;
Best Local Similarity 31.0%; Pred. No. 8.6e-38;
Matches 226; Conservative 118; Mismatches 264; Indels 122; Gaps 33;
QY 3 KMSPYQNKNEVEILLESSNNNTNTPRYFPANNRDMSTWSDCQGISWDEIWE---SVET 59
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 20 KISTDSLKNETDI-----ELQNIHEDCLKMSYENVPEPVSAST 59
60 I-TSIGI--NLIEFVIEPSLGGINTLLS--IIGKLIPTNRQTVSALSICDILLSIRKEVAD 115
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 60 IQTGIGIAGKILGTGVFPAGQIASLYSFLGELWPKGKQWE--IFMEHVEEIIQKIST 118
116 SVLSDAIADPDGKLNRYREYLYSLGAWLKDGKPLQKTNNSDIOQLV--YFVKLSRDPN 173
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 119 YARNKALTDLKG--LGDALAVYHDSLESWGN-----RNNTRARSVVKQYIAL--ELMFV 170
174 EILGSLSRNAOVLLLPFAQAAVQLLLRDVAVQYKAQWPFPLSAENVSELISPNSG 233
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 171 QKL--PSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW--GLSSASEIST----- 219
234 CDFTGDIYERLCKTAETNYCLYQVGLNQIKQGGTGADTWKSKFRRREMTLAVLDI 293
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 220 -----FYNQOVERAGDYSYHCVKYSTGLNLR--GTWAKSWVRNQPKDMLNVLDL 271
294 IAIPTPYDEKYPPLPHVELTREIYTDVG-----YSSGTYSWLRNWPNTFNGLEANG 346
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 272 VALFPSYDQVPIKTTAQLTREYVTDAGTVHPNQAFASFT--WYNNNAPSFAIEAAV 329
347 TRGCLVWLSKIGIYNEVSR-----YFAGWVGTRHYEDYTKNGIFORMSGTTSNDLR 401
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 330 VRNPHLLDFLQSVTIYS--LLSRWSNTQYNNMGHGR--LESRRPIGGALNTSTQGSTNT 387
402 --NIDFQNAVYKITSLAIMNLVGETTARPEYRSKADF--RRVGGP---DLNYDAGNNG 454
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 398 PVLTPFTSRDVRVRYTESLAGLNF--LTPVNGVPRVDFHMKFVTHPIASDNFYIYG 444
455 LSRMTIESTFPLVLHSG--VRGPHRLSNAACVYVGNRSRVNVTGHTSLKRENIIEA 511
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 445 IGTQLQDSENELPPEATGPQNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNTEP 504
512 NOIQIPAKSVYLYQNYLANAYTVIKGT--HTGGDLIRFLRTKSEYNVAVAGGIRLIN 570
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 505 NSITQIPLKAFNLSSGAA-----VVRGPGFTGGDLIRRTNTGT-----FGDIRVIN 552
571 NKTAGQSYRIRFRYAADKAFFSVLYPGGWSNRFRVLSKYSYGN-----DDLKYS 623
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 553 PPFA--QRYVRIRYASTTDLQFHTSI--NGKAIQ-----GNFSATWNRGDLDYK 600
624 DPKFAEIIITPPLPSSNIQMDVEMQANSFQSDVNVLDKIEFLPSTNTTLEYEGERDL 683
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 601 TERTVG--FTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVT---YEAEDFPEKA 656
684 KNAVNDLFTN 693
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 657 QEKVTAFTS 666

RESULT 7

S25383
parasporal crystal protein cryIIa1 - *Bacillus thuringiensis*
N:Alternate names: delta-endotoxin; parasporal crystal protein cryV
C:Species: *Bacillus thuringiensis*
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C:Accession: S25383
R:Tailor, R.; Tippett, J.; Gibb, G.; Pelli, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A>Title: Identification and characterization of a novel *Bacillus thuringiensis* delta-endotoxin
A:Reference number: S25383; MUID:92269582; PMID:1588820
A:Accession: S25383
A:Molecule type: DNA
A:Residues: 1-719 <TAI>
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI000002DB73; EMBL:X62821; NID:G40289; PID:

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QY 70 FVI-----EPSIGGINTLLS-IIGKLIPTNRQTVSALSICDILLSIRKEVADSLDAIAD 124
Db 60 RIIGLVGPAGQVASYSLVGLBPRGRDQWE-IFLEHVEQLNQIITENARNTALAR 118
QY 125 FDGKLKNRYEYLYSLGAWLKDGKPLQKTNNSDIGQLVY--YFKLSERDFNEILGGSLSR 182
Db 119 LQGLGDSFRAYQQS-LEDW-----LENRDDARTSRVLYTYQYIAL-ELDFLNAMPLFAIR 170
QY 183 NNAQVLLPTFAQAANVQLLLRDVAVQYKAQWFFFLSAENVRSELISPNSGCFTGDYYE 242
Db 171 NQ-EVPLLMVYAQAANLHLLLRDASLFGSE-FGLTSQEIQR-----YYE 213
QY 243 RLAKCKTAETNYCLYVYQVGLNQIKOGGTGADTWSKENKRRERMTLAVLDIIAIFPTDYF 302
Db 214 QOVERTRDYSIDYCVIEWTNTGLNSR--GTNAASWVRYNQPRDLTLGLVDLVALFPESYDT 271
QY 303 EKYPLPHTVELTREIYTDVAV---GYSGTYSWLRNMPNTENGLEANGTRGPGVLVWLSKI 359
Db 272 RTYPINTSAQLTREIVYTDALGATGVNMAWMNWNNAAPSASEAAIRSPHLLDFLEQL 331
QY 360 GIYNEVSVRFAGVGRHRYEDYTKGNIGIFORMSG-----TTSNDLRNIDFQNA 408
Db 332 TIFSA-----SSRWSNTRHM-TYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFASR 385
QY 409 DVYKITSLAIMNLVGETTARPEYRVSKADPRRVGGPDLDNYDAG-----NNGLSRMT 459
Db 386 DVTRTESYAGVLWG-IYLEPIHGVPTVRFNFTNPQNIS--DRGTANYSQPYESPGLQLKD 443
QY 460 IESTF-PLVLHSGVRGSPHRLSNAACVYVGNRSRVNVYGTWHTSLKRENIIEANQITQIP 518
Db 444 SETELPPTETTERPNYSYSHRLSHIGIILQSRVNVVPVSWTHRSADRTWTIGPNRIIQIP 503
QY 519 AVKSYVLYQNLANYTVYIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIINNKTAGOS 577
Db 504 MVRASELPQ-----GTTVVRGPGFTGGDILR--RTWTG-----GFGPIRVTVNGPLT-QR 550
QY 578 YRIRFYAADKAAPFSVLYPGWGSNRPVLSLEKSYSGNYDILKYSDFAEIIITPLPS 637
Db 551 YRIGFYAS--TVDFOFFVSRGGTTVNNRFLRTMNSG--DELKYGNF-VRRAFITPPTFF 605
QY 638 SNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTILEYEGERDLEKTKNAVNDLFTN 693
Db 606 TQIQDIIRTSIQLSGNGEVYIDKIIIP---VTATFEAYDLERAQEAVALFTN 658

RESULT 4
I39815
insecticidal protein cryV - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
C:Accession: I39815
R:Gleave, A.P.; Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1993
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for
iensis subsp. kurstaki.
A:Reference number: I39815; MUID:93298009; PMID:8517758
A:Accession: I39815
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45752; UNIPARC:UPI0000036008; GB:M98544; NID:gl42767; PIDN:
C:Gene: cryV
C:Superfamily: Parasporal crystal protein
Query Match 18.6%; Score 679; DB 2; Length 719;
Best Local Similarity 31.0%; Pred. No. 5.4e-38;
Matches 226; Conservative 119; Mismatches 263; Indels 122; Gaps 33;
QY 3 KMSYPQKNKNEYILESSNNNTNTPNRYPFANNRDMSTMSWNCQGISWDEIWE---SVET 59
Db 20 KISTDSLKNETDI-----ELQNIHNECDLKMSEYENVPEFVSAST 59
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QY 60 I-TSIOI--NLIEFVIEPSLGGINTLLS-IIGKLIPTNRQTVSALSICDILLSIRKEVAD 115
Db 60 IQTGIGIAGIKLGTGLVPPAGQVASYSLFGLBWPKGKNQWE-IFMEHVEEIIINOKIST 118
QY 116 SVLSDAIADPDGKLNRYEYLYSLGAWLKDGKPLQKTNNSDIGQLV--YVFKLSERDFN 173
Db 119 YARNKALTDLKG-LGDALAVYHDSLSWVGN-----RNNTRARSVVKSYQYIAL-ELMPV 170
QY 174 EILGGSLSRNNAQVLLPTFAQAANVQLLLRDVAVQYKAQWFFFLSAENVRSELISPNSG 233
Db 171 OKL-PSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW--GLSSSEIST----- 219
QY 234 CDFTGDYERLCKTAETNYCLYVYQVGLNQIKOGGTGADTWSKENKRRERMTLAVLDI 293
Db 220 -----FYNRQVERAGDYSCHCKWYSTGLNNLR--GTNAESWVRYNQPRDRDTLMVLDL 271
QY 294 IAIPTDYDEKYPPLPHTVELTREIYTDVAV-----YSSGTYSWLRNMPNTENGLEANG 346
Db 272 VALFPSTYDQMTPIKTTAQLTREIVYTDALGTVHPHPSFTT--WYNNNAPSFSAIEAAV 339
QY 347 TRGPGVLVWLSKIGIYNEYSR-----YPAGVWGRHRYEDYTKGNIGIFORMSGTTSNDLR 401
Db 330 VRNPHLLDLEQVTIYS-LLSRWSNTQYNNMW-GGHKLEFRTIGGTINISTQGSTWTSIN 387
QY 402 --NIDFQNDVYKITSLAIMNLVGETTARPEYRVSKADF--RRVGGP-----DLNYDAGNNG 454
Db 388 PVTLPFTSRDVRTTESLAGNLF--LTQPVNGVPRVDFHWKFPVTHPIASDNPFPYPGYAG 444
QY 455 LSRMTIESFPFLVLHNSG---VRGSPHRLSNAACVYVGNRSRVNVYGTWHTSLKRENIIEA 511
Db 445 ICTQIQDSNELPPTATGQPNYESYSHRLSHIGLSASHVKALVSWTHRSADRTWTIEP 504
QY 512 NQITQIPAVKSYVLYQNLANYTVYIKGT-HTGGDLIRFLRTKSEYNAVYAGGIRLIIN 570
Db 505 NSITQIPLVKAFNLSSGAA-----VVRGPGFTGGDILRETNGT-----FGDIRVIN 552
QY 571 NKTACQSVIRIRPYAADKAAPFSVLYPGWGSNRPVLSLEKSYSGNY-----DDLKYS 623
Db 553 PPFA-QRYVRVIRYASTTDLPHTSIT--NGKAINQ-----GNFSATMNRGEDLDYK 600
QY 624 DPKFAEIIITPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTILEYEGERDLEKT 683
Db 601 TPTVTG-FTTPPSFLDVQSTFTTIGAWNFSSGNEVIDRIEFVPEVET-----YEAEDFEKA 656
QY 684 KNVAVNDLFTN 693
Db 657 QEKVTALFTS 666

RESULT 5
I40590
cryV465 protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
C:Accession: I40590
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I40590
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45709; UNIPARC:UPI000003600C; EMBL:U07642; NID:g467234; PI:
C:Gene: cryV465
C:Superfamily: Parasporal crystal protein
Query Match 18.6%; Score 678.5; DB 2; Length 719;
Best Local Similarity 30.8%; Pred. No. 5.8e-38;
Matches 226; Conservative 119; Mismatches 281; Indels 107; Gaps 31;
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177 ---GSLSRNAQVLLPTFAQANVOLLIRDAVOYKAQW-----FPFLSAENVRSLEI 228
175 LTNGSLARQNAQVLLPTFAQANVOLLIRDAVOYKAQW-----FPFLSAENVRSLEI 234
229 SPNSGCDFTGDIYERLCKTAETNYCLYVYQVGLNQIKQGGTADTWKFNKFRREMTL 288
235 E-----LYTDYCVHYNRGNFELRQGTGSATAWLEFHYRREMTL 274
289 AVLDIIAIPDYDEKYPPLTHVELTREIYTDVAGY-----SGGTYSWLRL--NWPNTFNL 342
275 MVLDIVASFSSLDITNYPETDQLSRVIYTDPIGFVHRSSLRGSEWFSFVNAN--FSDL 333
343 EANGTRGGLVTLWSKIGIYNEVSRYPAG-----WVGRHYEDYTKNGIFQBMST 395
334 E-NAIENPRPSWFLNNWISTGSLTLPVSPSTRARVWYGSRRDISPANSQFTELISQ 392
396 TSNLDNRIDFQADVYKITSALIMNLVGETTARPEYRVSADFRVGGPDLNVDAGNGL 455
393 HTATQTILGRN--IFRVDQA--CNL-NDTT---YGNRAVP-----YHDASEGS 435
456 SMTIESTPLVLHNSGVGPP-----SHRLSNAACVYVG-----489
436 QRSVYEG---YRTTGIDNPRVQNTYLPGENSDIPTPEDVTHILSTTINLTGLRQV 491
490 ---NSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYLQVLANAYTVYVKGTHGTD 545
492 ASNRSSLYVYGTWHTSLKRENIIEANQITQIPAVKSYLQVLANAYTVYVKGTHGTD 547
546 LIRFLRTKSEYNAVAGGGIRLIIINNTAGQSYRIRFRYAADKAAPFVSYLPGGWSNR 605
548 LLQ-----RTDHGSL-----GVLRVQFPLHLRQYRIRVRYASTNIRLSV-----NGS 591
606 FVSLKSYSGNY---DDLKYSDFKFAEIIITPPLP--SSNTQDMVEMQANSFQSDVNVLDK 661
592 FGTISQNLPSMTWRLGSDLYGSFAIREFNTSIRTPASPDQIRLTIEPSIRQEVYV--DR 649
662 IEFLPSNTTILEYGERDLKTKNAVNDLFT 692
650 IEFIPVNPTR---EAKEDLEAAKAVASLFT 677

RESULT 2
140589
parasporal crystal protein cry8Cal - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cryIII
C:Species: Bacillus thuringiensis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
C:Accession: I40589
R:Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano
Curr. Microbiol. 28, 15-19, 1994
A:Title: Cloning, heterologous expression, and localization of a novel crystal protein g
A:Reference number: I40589; MUID:94100786; PMID:7764305
A:Accession: I40589
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1160 <RES>
A:Cross-references: UNIPROT:Q45706; UNIPARC:UPI0000126CPE; EMBL:U04366; NID:G532523; PID
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 19.9%; Score 728.5; DB 2; Length 1160;
Best Local Similarity 29.9%; Pred. No. 4.7e-41;
Matches 232; Conservative 124; Mismatches 240; Indels 179; Gaps 34;
4 MSPYQNKNEYIELESSNNTNPN--RYPFANNRDMSTMSWDCQISWDE-----52
1 MSP-NNQNEYIIDLSPVSNSIRYPLANDQNTLQNMKYKYLKMTSTNAELSRN 59
53 --IWSEVETITIGINLIEFVIE-----PSLGGINTLL-SIIGKLIPTNROTYSALSICDL 105
60 PGTIFISAQAVGTGIDIVTISGLGIPVLGEVFSILGSLIGLLWPSNNENWQIFMNRV 119

106 LSIIRKEVADSVLSDAIADFDGKLKNYR---EYLSYLGAWLKDGKPLQKTNNSDIGQLV 162
120 BELIDQKILDSVRSALAD---LANSRIAVEYYQNALEDWRKNP---HSTRSAAL---- 168
163 YFVKLSERDFN--ETLG---GSLSRNAQVLLPTFAQANVOLLIRDAVOYKAQWPPF 217
169 ---VKEFGNAELRLTNMGFSQNTYETPLPTFAQANVOLLIRDAVOYKAQWPPF 222
218 LSAENVRSLEI--SPNSGCDFTGDIYERLCKTAETNYCLYVYQVGLNQIKQGGTADTW 277
223 ---YQNDIDL---FYKEQVSYTARYSDHCVQWYNAGLNKLRL--GTGAKQWV 266
278 KFNKRRRMTLAVLDIIAIPDYDEKYPPLTHVELTREIYTDVAGY-----SGGTYSWLRLNWP 336
267 DYNFRFRMNVMVLDLVALFPNYDARIYPLETNAELTREIETDPVGSVYVTCQSSTLSWY 326
337 N-----TFNGLEANGTRGGLVTLWSKIGIYNEV---VSRYPAGWVGTRHYEDYTKG 385
327 DMIPALPSPSTLE-NLLRKPDFFLLQEIEMYSFRONGTIEYNYVGGQRLTSLYIG 385
386 NGIFORMSGTNSDLNRIDFQADVYK-----TSALIMNLVGETTAR 428
386 SS-FNKYSGLVAGAEIIPVQNDIYRVVTVIGRYTNSLLGVNPDVTFVSNNTQKTSK 444
429 PEY---RVSKADFRVGGPDL---NYDAGNGLSRMT---TESTPPLVLHNSGVGPPSHR 479
445 PKQAGGKTKTD---SGBELTYENQSYSHRVSYSITSFEIKSTGGTVL---GV-----491
480 LSNACVYGVGNSRVNVYGTWHTSLKRENIIEANQITQIPAVKSYLQVLANAYTVYVKG 539
492 ---VPIFGWTHSSASRNFIYATKLSQIPINKA---SRTSGAVNWFQEG 535
540 THTGDLRLIRUTKSEYNAVAGGG-----IRLIINNTAGQSYRIRFRYAADKAAPFVS 594
536 LYNGGPNVVKL-----SGSGSVINLRVATDAKAGSQRYRIRIRYASDRAGKFTI 584
595 YLPGGWSNRVSLKSYSGNY-----DDLKYSDFKFAEIIITPPLSSNTQDMVE 645
585 ---SSRSPENPATYSASIAVTNTMTSNASLTYSTPAYAE-----SGPINLGIS 629
646 MQANSFQSDV-----NVLDKIEFLPSNTTILEYGERDLKTKNAVNDLFTN 693
630 GSSRTFDLSITKEAGANLYIDRIEIPVNTL---FEAEEDLDVAKAVGLFTN 681

RESULT 3
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: parasporal crystal protein cryA4
C:Species: Bacillus thuringiensis subsp. thuringiensis
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Oct-2004
C:Accession: S00873
R:Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; UNIPARC:UPI0000126BDC; EMBL:X06711; NID:G40264; PIDN
C:Genetics:
A:Gene: cryA4
A:Start codon: TTG
C:Superfamily: Parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 19.3%; Score 705.5; DB 2; Length 1228;
Best Local Similarity 31.3%; Pred. No. 1.9e-39;
Matches 224; Conservative 118; Mismatches 279; Indels 95; Gaps 31;
10 KNEVEILSSNNTNPNRYFANNRDMSTMSWDCQISWDEIWESVETITIGINLIE 69
6 KNEEINAVNHSNQMDLLPDARIEDSLCTA---EGNNIDP-FVSASTVQT-GINTAG 59

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2005, 11:08:56 ; Search time 43 Seconds
(without alignments)

1550.656 Million cell updates/sec

Title: US-10-781-979-3

Perfect score: 3655

Sequence: 1 MKQMSPYQNKNEYEILLESSS.....YEGERDLEKXNAVNDLFTN 693

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: Pirt1:*

2: Pirt2:*

3: Pirt3:*

4: Pirt4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	20.4	1156	2 S19306	parasporal crystal
2	728.5	19.9	1160	2 I40589	parasporal crystal
3	705.5	19.3	1228	2 S00873	parasporal crystal
4	679	18.6	719	2 I39815	insecticidal prote
5	678.5	18.6	719	2 I40590	cryV465 protein -
6	676	18.5	719	2 I39814	insecticidal prote
7	676	18.5	719	2 S25383	parasporal crystal
8	636	17.4	659	2 S10228	parasporal crystal
9	631.5	17.3	652	2 A27323	parasporal crystal
10	617.5	16.9	934	2 B29838	parasporal crystal
11	609	16.7	649	1 JH0261	parasporal crystal
12	606.5	16.6	1180	2 A26858	parasporal crystal
13	605.5	16.6	1180	2 I39870	parasporal crystal
14	605	16.6	652	2 I39811	parasporal crystal
15	603.5	16.5	1154	2 S39536	parasporal crystal
16	585.5	16.0	1138	2 A48944	parasporal crystal
17	578	15.8	1136	1 USB881	parasporal crystal
18	554.5	15.2	1157	1 S49247	parasporal crystal
19	547.5	15.0	1166	2 S32645	parasporal crystal
20	542	14.8	1172	2 S32649	parasporal crystal
21	542	14.8	1178	1 USB8XH	parasporal crystal
22	540.5	14.8	1177	2 A49785	parasporal crystal
23	530	14.5	934	2 A22798	parasporal crystal
24	530	14.5	1176	2 A22617	parasporal crystal
25	530	14.5	1176	2 JC2219	parasporal crystal
26	530	14.5	1176	2 S02215	parasporal crystal
27	529.5	14.5	1155	2 I39838	parasporal crystal
28	528	14.4	1176	2 JT0241	parasporal crystal
29	525.5	14.4	1174	2 A42459	parasporal crystal

30	523.5	14.3	1155	2 JD0002	parasporal crystal
31	523.5	14.3	1156	2 A29125	parasporal crystal
32	522.5	14.3	1155	2 S02134	parasporal crystal
33	522	14.3	1181	2 A41052	parasporal crystal
34	521.5	14.3	1155	2 A26513	parasporal crystal
35	520.5	14.2	1165	2 S11446	parasporal crystal
36	517.5	14.2	1176	2 A48970	parasporal crystal
37	515.5	14.1	618	2 S11445	parasporal crystal
38	511	14.0	823	2 S04181	parasporal crystal
39	506.5	13.9	1160	2 S32647	parasporal crystal
40	499	13.7	655	2 JC7140	protoxin - Bacillu
41	497	13.6	1156	2 A29838	parasporal crystal
42	488	13.4	1171	2 A37829	parasporal crystal
43	488	13.4	1171	2 I40572	parasporal crystal
44	488	13.4	1189	2 S00944	parasporal crystal
45	473.5	13.0	1172	2 S32689	parasporal crystal

ALIGNMENTS

RESULT 1

S19306

parasporal crystal protein cry9Aa1 - Bacillus thuringiensis

N;Alternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal pr

C;Species: Bacillus thuringiensis

C;Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 05-Oct-2004

C;Accession: S19306; S23588; A44847; S14837

R;Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyr

FEBS Lett. 293, 25-28, 1991

A;Title: Nucleotide sequence of a novel delta-endotoxin gene cryIg of Bacillus thuringi

A;Reference number: S19306; MUID:92070568; PMID:1660003

A;Accession: S19306

A;Molecule type: DNA

A;Residues: 1-1156 <SMU>

A;Cross-references: UNIPROT:Q99031; UNIPARC:UPI0000126D09; EMBL:X58120; NID:g870929; PI

A;Experimental source: subsp. galleriae

A;Accession: S23588

A;Molecule type: protein

A;Residues: 24-34 <SMUI>

A;Cross-references: UNIPARC:UPI00001781A2

A;Experimental source: subsp. galleriae

R;Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.

J. Gen. Microbiol. 138, 55-62, 1992

A;Title: Identification of an insecticidal crystal protein from Bacillus thuringiensis I

A;Reference number: A44847; MUID:92211329; PMID:1556556

A;Accession: A44847

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1151 <GLE>

A;Cross-references: UNIPARC:UPI000016EA36; EMBL:X58534; NID:g48879; PIDN:CAA41425.1; PI

A;Experimental source: isolate DSIR517

A;Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBIPI:92867)

C;Genetics:

A;Gene: cryIG

C;Superfamily: Parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 20.4%; Score 747; DB 2; Length 1156;
Best Local Similarity 30.6%; Pred. No. 2.6e-42;
Matches 230; Conservative 130; Mismatches 249; Indels 142; Gaps 31;

QY 9 NKNEYEILLESSNNNTTFN--RYPPANNRDMTSMWNCQG---ISW-DEIWESVETITS 62

Db 2 NQKHGIIGASCGCASDDVAKYPLANNPYSSALNLSQNSILNWINIIGDAAKEAVS 61

QY 63 IGINLIEFVIEPSLCG-INLLSIIIGKLI-PNRTQVTSALSDLLSIIKRVASVLS 120

Db 62 IGTTLVSLITAPSLTGLISIVVDLIGKLVGGSGSISDLSDLLSIIKRVASVLS 121

QY 121 ATADFDGKLNKRYEYLVGLAWLKDGPLOKTNNSDIGLVYVFKLSRDRNEIL---- 176

Db 122 GIADPNGSVLLYRN-YLEALDSWNKN-----PNSASAEELTRPRIADSEFDRLTRGS 174